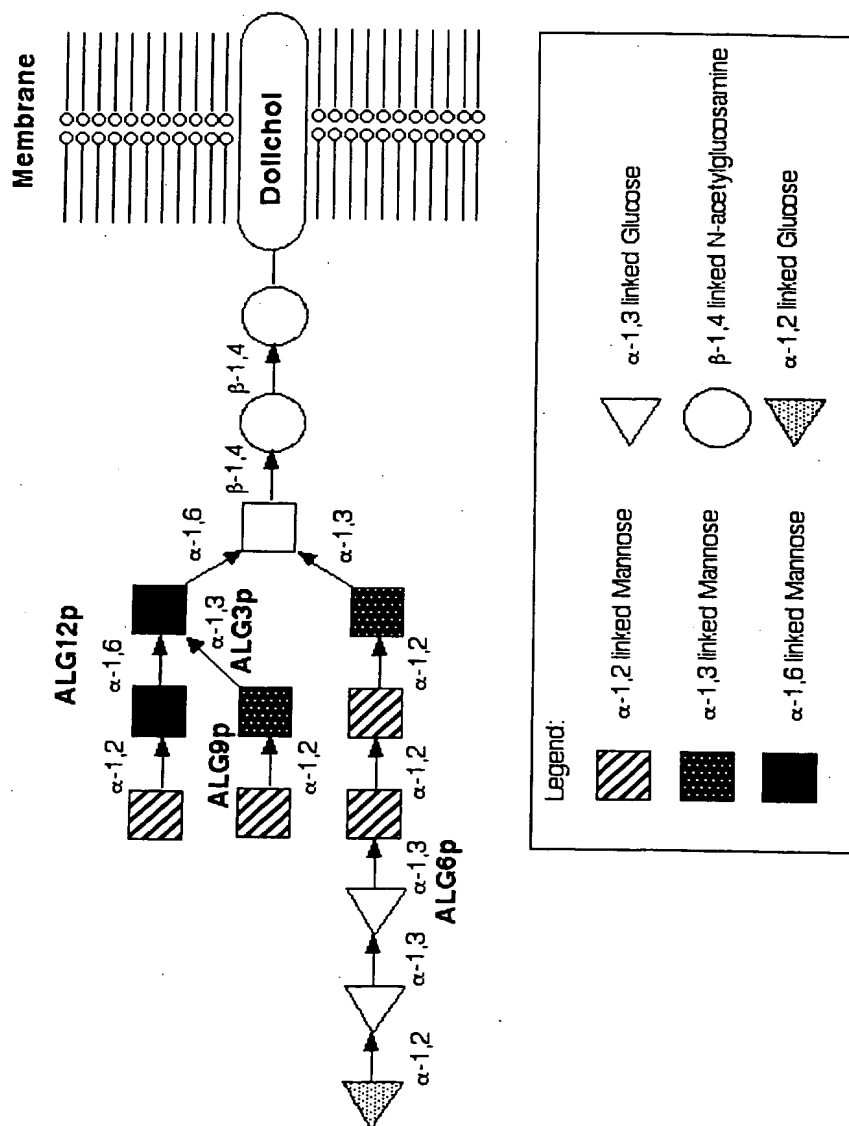


10/500240

FIGURE 1



Lipid-linked N-glycans

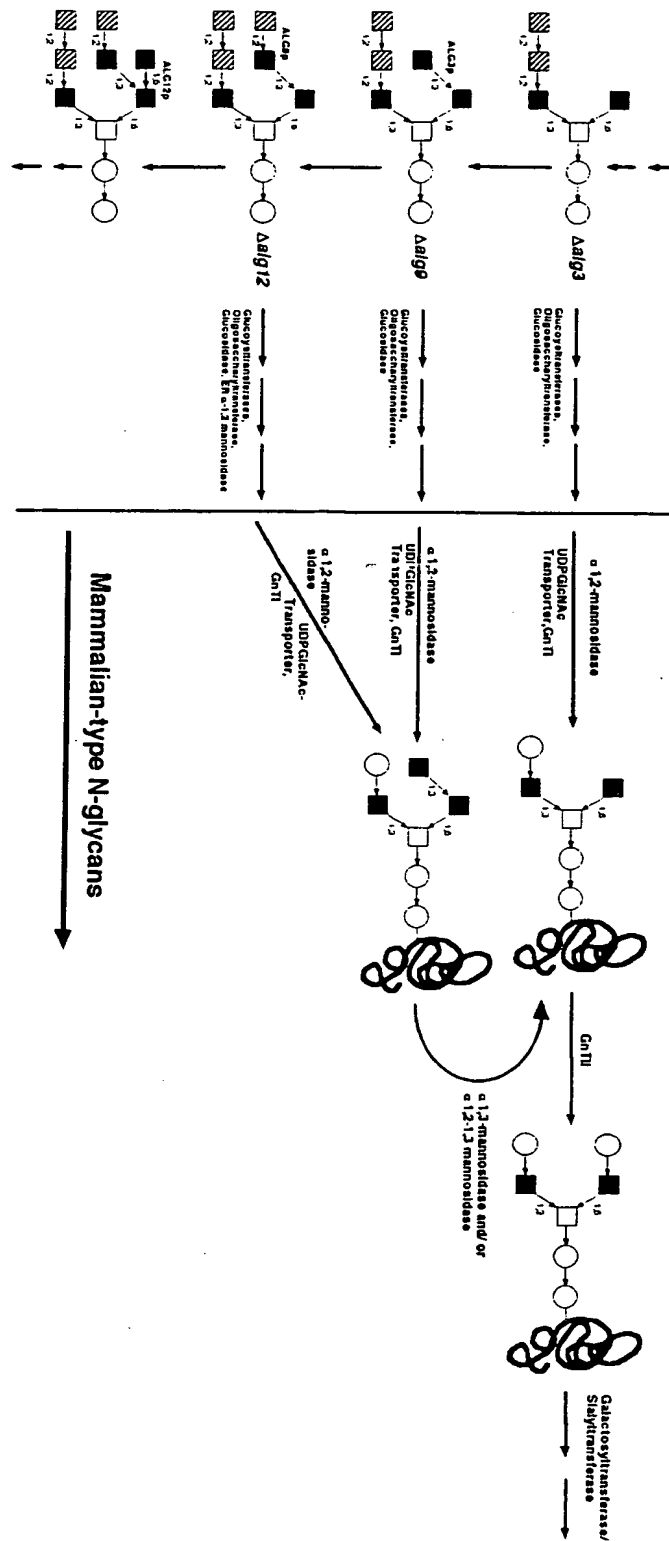


FIGURE 2

FIGURE 3

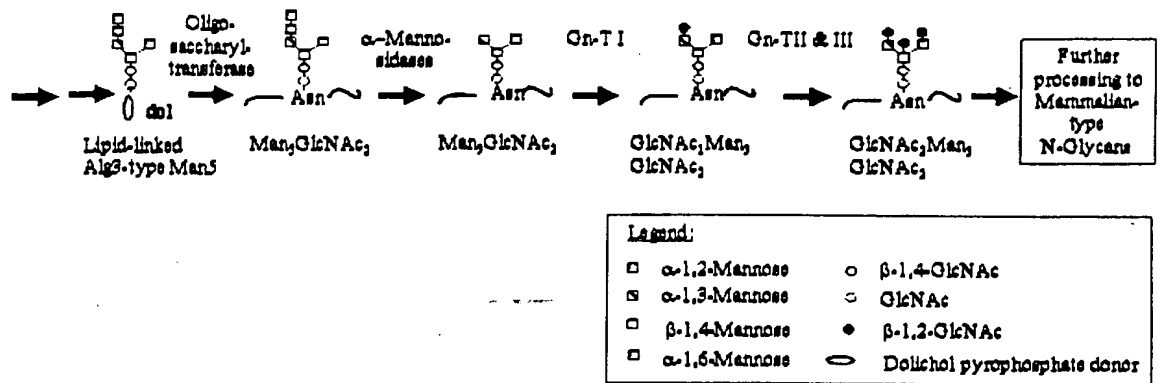


FIGURE 4 (sheet 1)

ALG3 Blast 05-22-01

Sequences producing significant alignments: (bits) Value

gi 586444 sp P38179 ALG3_YEAST	DOLICHYL-P-MAN:MAN(5)GLCNAC(...797	0.0
gi 3024226 sp Q92685 ALG3_HUMAN	DOLICHYL-P-MAN:MAN(5)GLCNAC...173	7e-43
gi 3024221 sp Q24332 NT56_DROVI	LETHAL(2)NEIGHBOUR OF TID P...145	3e-34
gi 3024222 sp Q27333 NT56_DROME	LETHAL(2)NEIGHBOUR OF TID P...121	3e-27
gi 10720153 sp P82149 NT53_DROME	LETHAL(2)NEIGHBOUR OF TID ...121	5e-27
gi 1707982 sp P40989 GLS2_YEAST	1,3-BETA-GLUCAN SYNTHASE CO... 32	2.8
gi 1346146 sp P38631 GLS1_YEAST	1,3-BETA-GLUCAN SYNTHASE CO... 31	6.6

Alignments

Yeast

>gi|586444|sp|P38179|ALG3_YEAST DOLICHYL-P-MAN:MAN(5)GLCNAC(2)-PP-DOLICHYL MANNOSYLTRANSFERASE
 (DOL-P-MAN DEPENDENT ALPHA(1-3)-MANNOSYLTRANSFERASE)
 (HM-1 KILLER TOXIN RESISTANCE PROTEIN)
 Length = 458

Score = 797 bits (2059), Expect = 0.0
 Identities = 422/458 (92%), Positives = 422/458 (92%)

Query: 1	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYIFDCRANLIVMPLLILFESMLCKI	60
	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYIFDCRANLIVMPLLILFESMLCKI	
Sbjct: 1	MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYIFDCRANLIVMPLLILFESMLCKI	60
Query: 61	IIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGM	120
	IIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGM	
Sbjct: 61	IIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGM	120
Query: 121	DHVERGQVFFRYLYLLTLALQMACYLLHLPWCVVLACLSKRLHSIYVLRFLNDCFTTL	180
	DHVERGQVFFRYLYLLTLALQMACYLLHLPWCVVLACLSKRLHSIYVLRFLNDCFTTL	
Sbjct: 121	DHVERGQVFFRYLYLLTLALQMACYLLHLPWCVVLACLSKRLHSIYVLRFLNDCFTTL	180
Query: 181	FMVVTVLGAIVASRCHQRPKLKKSALVISATYSMAVSIKMNALLYFPAMMISLFILNDA	240
	FMVVTVLGAIVASRCHQRPKLKKSALVISATYSMAVSIKMNALLYFPAMMISLFILNDA	
Sbjct: 181	FMVVTVLGAIVASRCHQRPKLKKSALVISATYSMAVSIKMNALLYFPAMMISLFILNDA	240
Query: 241	NVILTLLDLVAMIAWQVAVAVPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEAFND	300
	NVILTLLDLVAMIAWQVAVAVPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEAFND	
Sbjct: 241	NVILTLLDLVAMIAWQVAVAVPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEAFND	300
Query: 301	KRFXXXXXXXXXXXXXXXXXVTRYPRILPDLWSSLCHPLRKNAVLNANPAKTIPFVLIASN	360
	KRF FVTRYPRILPDLWSSLCHPLRKNAVLNANPAKTIPFVLIASN	
Sbjct: 301	KRFHLALLISHLIALTTLFVTRYPRILPDLWSSLCHPLRKNAVLNANPAKTIPFVLIASN	360
Query: 361	FIGVLFPSRLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLHEWCWNSYPPNSQXXXXX	420
	FIGVLFPSRLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLHEWCWNSYPPNSQ	
Sbjct: 361	FIGVLFPSRLHYQFLSWYHWTLPILIFWSGMPFFVGPIWYVLHEWCWNSYPPNSQASTLL	420
Query: 421	XXXXXXXXXXXXXXXXXSGSVALAKSHLRTTSSMEKKLN	458
	SGSVALAKSHLRTTSSMEKKLN	
Sbjct: 421	LALNTVLLLLLALQLSGSVALAKSHLRTTSSMEKKLN	458

FIGURE 4 (sheet 2)

Human

>gi|3024226|sp|Q92685|ALG3_HUMAN DOLICHYL-P-MAN:MAN(5)GLCNAC(2)-PP-DOLICHYL
MANNOSYLTRANSFERASE

(DOL-P-MAN DEPENDENT ALPHA(1-3)-MANNOSYLTRANSFERASE)
(NOT56-LIKE PROTEIN)
Length = 438

Score = 173 bits (439), Expect = 7e-43
Identities = 133/396 (33%), Positives = 195/396 (48%), Gaps = 28/396 (7%)

Query: 26 WQDLKDGVRVIFDCRANLIVMPLLILFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLD 85
WQ+ R++R L+V LLE + +I +VAYTEID+KAYM ++E + ++
Sbjct: 29 WQER---RLLLREPRYTLLVAACLCLEAVGITFWVIHRVAYTEIDWKAYMAEVEGV-IN 83

Query: 86 GMLDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACY 145
G DY+Q+ G TGPLVYPAG V I+ +Y+ T + Q F LYL TL L Y
Sbjct: 84 GTYDYTQLQGDGTGPLVYPAGFVYIFMGLYYATSRGTDIRMAQNIFAVLYLATLLLVFLIY 143

Query: 146 Y-LLHLPWC-VVLACLSKRLHSIYVLRLENDCTTFLMVVTVLGAIVASRCHQRPKLKK 203
+ +PP+ + C S R+HSI+VLRLEND + + +L + QR
Sbjct: 144 HQTKVPPFVFFFMCCASYRVHSIFVLRLENDP-----VAMVLLFLSINLLLAQRWG- 197

Query: 204 SLALVISATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPF 263
+S+AVS+KMN LL+ P ++ L L L + A + QV + +PF
Sbjct: 198 -----CCFFSLAVSVKMNVLFPAGLLFLLLLTQFGFRGALPKLGICAGL--QVVLGLPF 249

Query: 264 LRSFPQQLHCAFNFRKFMYSINWQMMDEEAFNDKRFXXXXXXXXXXXXXXXXXFFVTRY 323
L P YL +F+ GR+F++ W++NW+ + E F + F + R+
Sbjct: 250 LLENPSGYLSRFDLGRQFLFHWTVNWRFLPEALFLHRAFLALLTAHLTLLLLFALCRW 309

Query: 324 PRILPDWSSLCHPLRKNVLANPAKTIPFVLIASNFIGVLFPSRSLHYQFLSWYHWTLP 383
R + S L P ++ I L SNFIG+ FSRSLHYQF WY TLP
Sbjct: 310 HRTGESILSLLRDPSKRKVPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYVWYFHTLP 369

Query: 384 ILIF----WSGMPFFVGPIWYVLHEWCWNSYPPNS 414
L++ W + + + E WN+YP S
Sbjct: 370 YLLWAMPARWLTHLLRLLVLGLI--ELSWNTYPSTS 403

Drosophila Vi

>gi|3024221|sp|Q24332|NT56_DROVI LETHAL(2)NEIGHBOUR OF TID PROTEIN (NOT58)
Length = 526

Score = 145 bits (366), Expect = 3e-34
Identities = 103/273 (37%), Positives = 157/273 (56%), Gaps = 17/273 (6%)

Query: 33 VRYVIFDCRANLIVMPLLILFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQ 92
++Y+ F+ A IV L++L E+++ ++I++V YTEID+KAYM++ E L+G +YS
Sbjct: 34 IKYLAFEPAALPIVSVLIVLAEAVINVLVIVRVPYTEIDWKAYMQECEGF-LNGTTNYSL 92

Query: 93 VSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACYLLH-LP 151
+ G TGPLVYPA V IY +Y+LT +V Q F +YLL + L + Y +P
Sbjct: 93 LRGDGTGPLVYPAAFVYIYSGLYLTGQGTNVRLAQYIFACIYLLQMCLVLRLYTKSRKVP 152

Query: 152 PWCVVLACL-SKRLHSIYVLRLENDCTTFLMVVTVLGAIVASRCHQRPKLKSLALVIS 210
P+ +VL+ S R+HSIYVLRLEND L +L A + QR L S
Sbjct: 153 PYVLVLSAFTSYRIHSIYVLRLENDPVAI-----LLYAALNLFQDQRTLG-----S 200

Query: 211 ATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPFLRSFPQ 270
YS+AV +KMN + A + LF L + V+ TL+ L Q+ + PFLR+ P +
Sbjct: 201 ICYSLAVGVKMN--ILLFAPALLLFYLANLGVRLTLVQLTICAVLQLFIGAPFLRTHPME 258

FIGURE 4 (sheet 3)

Query: 271 YLHCAFNFGRKFMYQWSINWQMMDEEAFNDKRF 303
 YL +F+ GR F ++W++N++ + +E F + F
 Sbjct: 259 YLRGSFDLGRIFEHKWTVNYRFLSKELFEQREF 291

Score = 53.3 bits (127), Expect = 1e-06
 Identities = 31/62 (50%), Positives = 41/62 (66%), Gaps = 6/62 (9%)

Query: 352 IPFVLIASNFIGVLFSRSLHYQFLSWYHWTLPILIFWSGMPFFVGPWIYVLH--EWCWNS 409
 +PF L NFIGV +RSLHYQF WY +LP L+ WS P+ +G + +L E+CWN+
 Sbjct: 412 LPFFL--CNFIGVACARSLHYQFYIWFHSLPYLV-WS-TPYSLGVRYLILGLIEYCWN 467

Query: 410 YP 411
 YP
 Sbjct: 468 YP 469

Drosophila melanogaster

>gi|3024222|sp|Q27333|NT56_DROME LETHAL(2)NEIGHBOUR OF TID PROTEIN (NOT56)
 (NOT45)

Length = 510

Score = 121 bits (305), Expect = 3e-27
 Identities = 96/272 (35%), Positives = 154/272 (56%), Gaps = 17/272 (6%)

Query: 34 RYVIFDCRANLIVMPLLLIFESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGMLDYSQV 93
 +Y++ + A IV ++L E ++ ++I++V YTEID+ AYM++ E L+G +YS +
 Sbjct: 36 KYLLEPAALPIVGLFVLLAELVINVVVIQRPVYTEIDWVAYMQECEGF-LNGTTNYSLL 94

Query: 94 SGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGOVFFRYLYLLTLALQMACYLLH-LPP 152
 G TGPLVYPA V IY +Y++T +V Q F +YLL LAL + Y +PP
 Sbjct: 95 RGDTPGLVYPAAFVYIYSALYYVTSHGNTVRLAQYIFAGIYLLQLALVLRLYSKSRKVPP 154

Query: 153 WCVVLACL-SKRLHSIYVLRFLFNDCTTLFMVVTVLGAIVASRCHQRPKLKSLALVISA 211
 + +VL+ S R+HSIYVLRFLFND + V +L A + +R L S
 Sbjct: 155 YVLVLSAFTSYRIHSIYVLRFLFNDP-----VAVLLLYAALNLFDRRWTLG-----ST 202

Query: 212 TYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVAVPFLRSFPQQY 271
 +S+AV +KMN + A + LF L + ++ T+L L Q+ + PFL + P +Y
 Sbjct: 203 FFSLAVGVKMN--ILLFAPALLLFYLANLGLLRTILQLAVCGVIQLLLGAPFLLTHPVEY 260

Query: 272 LHCAFNFGRKFMYQWSINWQMMDEEAFNDKRF 303
 L +F+ GR F ++W++N++ + + F ++ F
 Sbjct: 261 LRGSFDLGRIFEHKWTVNYRFLSRDVFENRTF 292

Score = 49.4 bits (117), Expect = 2e-05
 Identities = 27/60 (45%), Positives = 35/60 (58%), Gaps = 2/60 (3%)

Query: 352 IPFVLIASNFIGVLFSRSLHYQFLSWYHWTLPILIFWSGMPFFVGPWIYVLHEWCWNSYP 411
 +PF L N +GV SRSLSHYQF WY +LP L + + V + L E+CWN+YP
 Sbjct: 407 LPFFL--CNLVGVACSRSLHYQFYVWFHSLPYLAWSTPYSLGVRCILGLIEYCWN 464

FIGURE 4 (sheet 4)

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 28883317
Number of Sequences: 96469
Number of extensions: 1107545
Number of successful extensions: 2870
Number of sequences better than 10.0: 16
Number of HSP's better than 10.0 without gapping: 5
Number of HSP's successfully gapped in prelim test: 11
Number of HSP's that attempted gapping in prelim test: 2839
Number of HSP's gapped (non-prelim): 23

length of query: 458
length of database: 35,174,128
effective HSP length: 45
effective length of query: 413
effective length of database: 30,833,023
effective search space: 12734038499
effective search space used: 12734038499
T: 11
A: 40
X1: 15 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.8 bits)
S2: 67 (30.4 bits)

FIGURE 5

S. cerevisiae ALG3

ATGGAAGGTGAACAGTCTCCGCAAGGTGAAAAGTCTCTGCAAAGGAAGC
 AATTTGTCAGACCTCCGCTGGATCTGTGGCAGGATCTCAAGGACGGTGTG
 CGCTACGTGATCTTCGATTGTAGGGCCAATCTTATCGTTATGCCCCTTTTG
 ATTTTGTTCGAAAGCATGCTGTGCAAGATTATCATTAAAGAAGGTAGCTTAC
 ACAGAGATCGATTACAAGGCGTACATGGAGCAGATCGAGATGATTCAGCT
 CGATGGCATGCTGGACTACTCTCAGGTGAGTGGTGGAACGGGGCCCGCTGG
 TGTATCCAGCAGGCCACGTCTTGATCTACAAGATGATGTACTGGCTAACA
 GAGGGAATGGACCACGTTGAGCGCGGGCAAGTGTTTTTCAGATACTTGTA
 TCTCCTTACACTGGCGTTACAAATGGCGTGTTACTACCTTTTACATCTACC
 ACCGTGGTGTGTGGTCTTGGCGTGCCTCTCTAAAAGATTGCACTCTATTTA
 CGTGCTACGGTTATTCAATGATTGCTTCACTACTTTGTTTATGGTCGTCACG
 GTTTTGGGGGCTATCGTGGCCAGCAGGTGCCATCAGCGCCCCAAATTTAA
 GAAGTCCCTTGCGCTGGTGTATCTCCGCAACATACAGTATGGCTGTGAGCA
 TTAAGATGAATGCGCTGTTGTATTTCCCTGCAATGATGATTTCTCTATTTCAT
 CCTTAATGACGCGAACGTAATCCTTACTTTGTTGGATCTCGTTGCGATGAT
 TGCATGGCAAGTCGCAGTTGCAGTGCCCTTCTGCGCAGCTTTCCGCAACA
 GTACCTGCATTGCGCTTTTAATTTTCGGCAGGAAGTTTATGTACCAATGGAG
 TATCAATTGGCAAATGATGGATGAAGAGGCTTTCAATGATAAGAGGTTCC
 ACTTGGCCCTTTTAATCAGCCACCTGATAGCGCTCACCACTGTTTCGTCA
 CAAGATACCCTCGCATCCTGCCCCGATTTATGGTCTTCCCTGTGCCATCCGC
 TGAGGAAAAATGCAGTGCTCAATGCCAATCCCGCCAAGACTATTCCATTC
 GTTCTAATCGCATCCAACCTTCATCGGCGTCCTATTTTCAAGGTCCCTCCAC
 TACCAGTTTCTATCCTGGTATCACTGGACTTTGCCTATACTGATCTTTTGGT
 CGGGAATGCCCTTCTTCGTTGGTCCCATTTGGTACGTCTTGCACGAGTGGT
 GCTGGAATTCTATCCACCAAACTCACAAGCAAGCACGCTATTGTTGGCA
 TTGAATACTGTTCTGTTGCTTCTATTGGCCTTGACGCAGCTATCTGGTTCGG
 TCGCCCTCGCCAAAAGCCATCTTCGTACCACCAGCTCTATGGAAAAAAG
 CTCAACTGA

S. cerevisiae Alg3p

MEGEQSPQGEKSLQRKQFVRPPLDLWQDLKDGVRVYVIFDCRANLIVMPLLIL
 FESMLCKIIKKVAYTEIDYKAYMEQIEMIQLDGM LDYSQVSGGTGPLVYPAG
 HVLIYKMMYWLTEGMDHVERGQVFFRYLYLLTLALQMACYLLHLPPWCV
 VLACLSKRLHSIYVLRLFNDCFTTLFMVVTVLGAIVASRCHQRPKLKKSALV
 ISATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLVAMIAWQVAVA
 VPFLRSFPQQYLHCAFNFGRKFMYQWSINWQMMDEEAFNDKRFHLALLISHL
 IALTTLFVTRYPRILPDLWSSLCHPLRKNVNLNANPAKTIPFVLIASNFIGVLFS
 RSLHYQFLSWYHWTLPILIWWSGMPFFVGPIWYVLHEWCWNSYPPNSQASTL
 LLALNTVLLLLLALTQLSGSVALAKSHLRTTSSMEKKLN

FIGURE 6

P. pastoris ALG3

ATGCCTCCGATAGAGCCAGCTGAAAGGCCAAAGCTTACGCTGAAAAATGT
 TATCGGTGATCTAGTGGCTCTTATTCAAACGTTTTATTAAACCCAGATTTT
 AGTGTCTTCGTTGCACCTCTTTTATGGTTAGCTGATTCCATTGTTATCAAGG
 TGATCATTGGCACTGTTTCCTACACAGATATTGATTTTTCTTCATATATGCA
 ACAAATCTTTAAAATTTCGACAAGGAGAATTAGATTATAGCAACATATTTG
 GTGACACCGGTCCATTGGTTTACCCAGCCGGCCATGTTTCATGCTTACTCAG
 TACTTTTCGTGGTACAGTGATGGTGGAGAAGACGTCAGTTTCGTTCAACAA
 GCATTTGGTTGGTTATACCTAGGTTGCTTGTTACTATCCATCAGCTCCTACT
 TTTTCTCTGGCTTAGGGAAAATACCTCCGGTTTATTTTGTTTTGTTGGTAGC
 GTCCAAGAGACTGCATTCAATATTTGTATTGAGACTCTTCAATGACTGTTT
 AACAAACATTTTTGATGTTGGCAACTATAATCATCCTTCAACAAGCAAGTAG
 CTGGAGGAAAGATGGCACAACCTATTCATTATCTGTCCCTGATGCTGCAG
 ATACGTACAGTTTAGCCATCTCTGTAAAGATGAATGCGCTGCTATACCTCC
 CAGCATTCCCTACTACTCATATATCTCATTGTGACGAAAATTTGATTAAAG
 CCTTGGCACCTGTTCTAGTTTTGATATTGGTGCAAGTAGGAGTCGGTTATT
 CGTTCATTTTACCGTTGCACTATGATGATCAGGCAAATGAAATTCGTTCTG
 CCTACTTTAGACAGGCTTTTGACTTTAGTCGCCAATTTCTTTATAAGTGGA
 CGGTTAATTGGCGCTTTTTGAGCCAAGAACTTTCAACAATGTCCATTTTC
 ACCAGCTCCTGTTTGCTCTCCATATTATTACGTTAGTCTTGTTTCATCCTCAA
 GTTCCTCTCTCCTAAAAACATTGGAACCGCTTGGTAGATTTGTGTTGGA
 CATTTTCAAATTTTGGAAAGCCAACCTTATCTCCAACCAATATTATCAACGA
 CCCAGAAAGAAGCCCAGATTTTGTTTACACCGTCATGGCTACTACCAACTT
 AATAGGGGTGCTTTTTGCAAGATCTTTACACTACCAGTTCCTAAGCTGGTA
 TCGGTTCTCTTTGCCATATCTCCTTTACAAGGCTCGTCTGAACTTTATAGCA
 TCTATTATTGTTTATGCCGCTCACGAGTATTGCTGGTTGGTTTTCCAGCTA
 CAGAACAAAGTTCCGCGTTGTTGGTATCTATCTTACTACTTATCCTGATTC
 TCATTTTTACCAACGAACAGTTATTTCTTCTCAATCGGTCCCTGCAGAAA
 AAAAGAATACATAA

P. pastoris Alg3p

MPPIEPAERPRLTLKNVIGDLVALIQNVLFNPDFS VFVAPLLWLADSIVIKVIIG
 TVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAYSVLSWYS
 DGGEDVSFVQQAAGWLYLGCLLSISSYFFSGLGKIPPVYFVLLVASKRLHSIF
 VLRLFNDCLTTFLMLATHILQQASSWRKDGTTIPLSVPDAADTYSLAISVKMN
 ALLYLPAFLLLIYLICDENLIKALAPVLVLILVQVGVGYSFILPLHYDDQANEIR
 SAYFRQAFDFSQRQFLYKWTNVNWRFLSQETFNNVHFHQLLFALHIITLVLFILKF
 LSPKNIGKPLGRFVLDIFKFWKPTLSPTNIINDPERSPDFVYTVMATTNLIGVLF
 ARSLHYQFLSWYAFSLPYLLYKARLNFIASIIVYAAHEYCWLVFPATEQSSAL
 LVSILLILILIFTNEQLFPSQSVPAEKKNT

FIGURE 7 (sheet 1)

P. pastoris ALG3 BLAST

Sequences producing significant alignments: (bits) Value

gi 586444 sp P38179 ALG3 YEAST Dolichyl-P-Man:Man(5)GlcNAc(...228	2e-58
gi 12802365 gb AAK07848.1 AF309689.10 putative NOT-56 manno...212	8e-54
gi 984725 gb AAA75352.1 ORF 1 206	4e-52
gi 7492702 pir T39084 probable mannosyltransferase - fissi...176	8e-43
gi 16226531 gb AAL16193.1 AF428424.1 At2g47760/F17A22.15 [A...164	2e-39
gi 25367230 pir B84919 Not56-like protein [imported] - Ara...164	3e-39
gi 25814791 emb CAB70171.2 Hypothetical protein K09E4.2 [C...161	2e-38
gi 17535001 ref NP_496950.1 Putative plasma membrane membr...160	3e-38
gi 1654000 emb CAA70220.1 Not56-like protein [Homo sapiens...155	2e-36
gi 13279206 gb AAH04313.1 AAH04313 Unknown (protein for IMA...154	2e-36
gi 22122365 ref NP_666051.1 hypothetical protein MGC36684 ...150	3e-35
gi 21292031 gb EAA04176.1 agCP3388 [Anopheles gambiae str....120	4e-26
gi 1780792 emb CAA71167.1 lethal(2)neighbour of tid [Droso...114	3e-24

Alignments

S. cerevisiae

Score = 228 bits (580), Expect = 2e-58

Identities = 154/429 (35%), Positives = 229/429 (53%), Gaps = 37/429 (8%)

Query: 9 RPKLTLKNVIGDLVALIQNVLFNPDFS VFVAPLLWLADSIIVIKVIIGTVSYTDIDFSSYM 68
 RP L L DL ++ V+F+ ++ V PLL L +S++ K+II V+YT+ID+ +YM
 Sbjct: 20 RPPLDLWQ---DLKDGVRVYIFDCRANLIVMPLLILFESMLCKIIKKVAYTEIDYKAYM 76

Query: 69 QQIFKIR-QGELDYSNIFGDTGPLVYPAGHVHAYSVLSWYSDGGEDVSFVQQAFGWLYLG 127
 +QI I+ G LDYS + G TGPLVYPAGHV Y ++ W ++G + V Q F +LYL
 Sbjct: 77 EQIEMIQLDGM LDYSQVSGGTGPLVYPAGHVLIYKMMYWLTEGMDHVERGQVFFRYLYLL 136

Query: 128 CLLLSISSYFFSGLGKIPPVYFVLLVASKRLHSIFVLRLFNDCLTTFMLLATI---IILQ 184
 L L ++ Y+ L +PP VL SKRLHSI+VLRLFNDC TT M+ T+ I+
 Sbjct: 137 TLALQMACYY---LLHLPWCVVLA CLSKRLHSIYVLRLFNDCFTTLFMVVTVLGAIVAS 193

Query: 185 QASSWRKDGTTIPLSVPDAADTYS LAISVKMXXXXXXXXXXXXXXXXXCDENLIKALAPXX 244
 + K ++ L + + TYS+A+S+KMN D N+I L
 Sbjct: 194 RCHQRPKLKSLALVI---SATYSMAVSIKMNALLYFPAMMISLFILNDANVILTLLDLV 250

Query: 245 XXXXXXXXXXXYSFILPLHYDDQANEIRSAYFRQAFDFS RQFLYKWTVNWRFLSQETFNNV 304
 F+ Y AF+F R+F+Y+W++NW+ + +E FN+
 Sbjct: 251 AMIAWQVAVAVPFL-----RSFPQQLHCAFNFRKFMYSINWQMMDEEAFNDK 301

Query: 305 HFHQLLFALHIITL-VLFIKFLSPKNIGKPLGRFVLDFKFWKPTLSPTNIIN-DPERS 362
 FH L H+I L LF+ ++ R + D++ L ++N +P ++
 Sbjct: 302 RFHLALLISHLIALTTLFVTRY-----PRILPDLWSSLCHPLRKNVLANPNAKT 351

Query: 363 PDFVYTVMATTNLIGVLFARSLHYQFLSWYAFSLPYLLYKARLNFIASIIVYAAHEYCWL 422
 F V+ +N IGVLF+RSLHYQFLSWY ++LP L++ + + F I Y HE+CW
 Sbjct: 352 IPF---VLIASNFIGVLF SRSLHYQFLSWYHTLPILIFWSGMPFFVGPIWYVLHEWCWN 408

Query: 423 VFPATEQSS 431
 +P Q+S
 Sbjct: 409 SYPPNSQAS 417

FIGURE 7 (sheet 2)

Neurospora crassa

Score = 212 bits (540), Expect = 8e-54

Identities = 140/400 (35%), Positives = 212/400 (53%), Gaps = 29/400 (7%)

Query: 35 SVFVAPLLWLADSIVIKVIIGTVSYTDIDFSSYMQIFKIROGELDYSNIFGDTGPLVYP 94
S + P L+L D+++ +II V YT+ID+++YM+Q+ +I GE DY+ + G TGPLVYP

Sbjct: 33 SKLIPPALFLVDALLCGLIIVKVPYTEIDWAAAYMEQVSQILSGERDYTKVRGGTGPLVYP 92

Query: 95 AGHVHAYSVLSWYSDGGEDVSFVQQAAGWLYLGCLLLSISSYFFSGLGKIPPVYFVLLVA 154
A HV+ Y+ L +D G ++ QQ F LY+ L + + Y+ K PP F LL

Sbjct: 93 AAHVYIYTGLYHLTDEGRNILLAQQLFAGLYMVT LAVVMGCYW---QAKAPPYLFPLLTL 149

Query: 155 SKRLHSIFVLRFNDC + I Q+ +W+ A Y+L + VK 214
SKRLHSIFVLR FNDC + I Q+ +W+ A Y+L + VK

Sbjct: 150 SKRLHSIFVLRFCFND CFAVLFWLAIFFQFQ-RNWQA-----GALLYTLGLGVK 197

Query: 215 MNXXXXXXXXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXSYFILPLHYDDQANEIRSAY 274
M + + L F+ HY + Y

Sbjct: 198 MTL LLSLPAVGIVLFLGSG-SFVTTLQLVATMGLVQILIGVPFL--AHYPT-----Y 247

Query: 275 FRQAFDFSQFLYKWTNVNWRFLSQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGK 333
+AF+ SRQF +KWTNVNRF+ +E F + "F" L ALH++ L +FI +++ P K

Sbjct: 248 LSRAFELSRQFFFKWTNVNRFVGEIEFLSKGFALTLLALHVLVLGIFITTRWIKPAR--K 305

Query: 334 PLGRFVLDFKFWKPTLS-PTNIINDPERSPDFVYTMATTNLIGVLFARSLHYQFLSWY 392
L + + + KP L+ P + +P ++ T + + N +G+LFARSLHYQF ++

Sbjct: 306 SLVQLISPVLLAGKPPLTVPEHRAAARDVTPRYIMTTILSANAVGLL FARS LHYQFYAYV 365

Query: 393 AFSLPYLLYKARLNFIAIIIVYAAHEYCWLVFPATEQSSA 432
A+S P+LL++A L+ + +++A HE+ W VFP+T SSA

Sbjct: 366 AWSTPFLLRAGLHPVLVYLLWAVHEWAWNVPSTPASSA 405

Schizosaccharomyces pombe

Score = 176 bits (445), Expect = 8e-43

Identities = 132/390 (33%), Positives = 194/390 (49%), Gaps = 35/390 (8%)

Query: 42 LWLADSIVIKVIIGTVSYTDIDFSSYMQIFKIROGELDYSNIFGDTGPLVYPAGHVHAY 101
L L + + II V YT+ID+ +YM+Q+ GE DY ++ G TGPLVYP GHV Y

Sbjct: 30 LLLLEIPFVFAIISKVPYTEIDWIAIYMEQVNSFLLGERDYKSLVGCTGPLVYPGGHVFLY 89

Query: 102 SVLSWYSDGGEDVSFVQQAAGWLYLGCLLLSISSYFFSGLGKIPPVYFVLLVASKRLHSI 161
++L + +DGG ++ Q F ++Y + +I Y F + + P +VLL+ SKRLHSI

Sbjct: 90 TLLYYLTDGGTNIVRAQYIFAFVYW--ITTAIVGYL FK-IVRAPFYIYVLLILSKRLHSI 146

Query: 162 FVLRFLNDCLTTFMLLATIIILQASSWRKDGTTIPLSVPDAAADTYSLAISVKMNXXXXX 221
F+LRLFNDC + L + I+ W + A+ S+A SVKM+

Sbjct: 147 FILRFLNDCGFNS-LFSSLFILSSCKKKWVR-----ASILLSVACSVKMSSLLYV 194

Query: 222 XXXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXSYFILPLHYDDQANEIRSAYFRQAFDF 281
L++ L P + + + +Y+ QAFDF

Sbjct: 195 PAYLVL-----LLQILGPKKTWMHIFVIIIVQILFSIPF----LAYFWSYWTQAFDF 242

Query: 282 SRQFLYKWTNVNWRFLSQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGKPLGRFVLD 341
R F YKWTNVNRF+ + F + F + LH+ LV F K + + P

Sbjct: 243 GRAFDYKWTNVNWRFI PRSIFESTSFSTSILFLHVALLVAFTCKHWNKLSRATP----- 295

Query: 342 IFKFWKPTLSPTNIINDPERSPDFVYTMATTNLIGVLFARSLHYQFLSWYAFSLPYLLY 401
F L+ + +P+F++T.+AT+NLIG+L ARSLHYQF +W+A+ PYL Y

FIGURE 7 (sheet 3)

Sbjct: 296 -FAMVNSMLTLKPLPKLQLATPNFIFTALATSNLIGILCARSLHYQFYAWFAWYSPYLCY 354

Query: 402 KARLNFIASIIIVYAAHEYCWLVFPATEQSS 431
 +A I ++ EY W VFP+T+ SS

Sbjct: 355 QASFPAPIVIGLWMLQEYAWNVPSTKLSS 384
Arabidopsis thaliana

Score = 164 bits (415), Expect = 2e-39
 Identities = 131/391 (33%), Positives = 194/391 (49%), Gaps = 29/391 (7%)

Query: 42 LWLADSIIVIKVIIGTVSYTDIDFSSYMQQIFKIRQGELDYSNIFGDTGPLVYPAGHVHAY 101
 L LAD+I++ +II V YT ID+ +YM Q+ GE DY N+ GDTGPLVYPAG ++ Y

Sbjct: 39 LILADAILVALIIAYVPYTKIDWDAYMSQVSGFLGGERDYGNLKGGDTGPLVYPAGFLYVY 98

Query: 102 SVLSWYSDDGGEDVSFVQQAFGWLYLGCLLSISSYFFSGLGKIPPVYFVLLVASKRLHSI 161
 S + + G +V Q FG LY+ L + + Y + + +P LL SKR+HSI

Sbjct: 99 SAVQNLTGG--EVYPAQILFGVLYIVNLGIVLIIYVKTDV--VPWWALSLLCLSKRIHSI 154

Query: 162 FVLRLFNDCLTTFMLLATIIILQQASSWRKDGTTIPLSVDAADTYSLAISVKMNNXXXXX 221
 FVLRLFNDC L+ A++ + +RK + + +S A+SVKMN

Sbjct: 155 FVLRLFNDCFAMTLLHASMAFL----YRKWHLGMLV-----FSGAVSVKMNVLLEYA 202

Query: 222 XXXXXXXXXXXCDENLIKALAPXXXXXXXXXXXXXSYFILPLHYDDQANEIRSAYFRQAFDF 281
 N+I ++ F++ +Y AFD

Sbjct: 203 PTLLLLLLKAM--NIIGVVSALAGAALQILVGLPFLITYPV-----SYIANAFDL 251

Query: 282 SRQFLYKWTNVNRFLSQETFNNVHFHQLLFALHIITLVLFILKFLSPKNIGKPLGRFVLD 341
 R F++ W+VN++F+ + F + F L H+ LV F + K+ G +G

Sbjct: 252 GRVFIHFWSVNFKFVPERVFSKEFAVCLLIAHLFLLVAFA-NYKWCKHEGGIIGFMRSR 310

Query: 342 IFKFWKP-TLSPTNIINDPERSPDFVYTMATTNIGVLFARSLHYQFLSWYAFSLPYLL 400
 F P +LS +++ + + V T M N IG++FARSLHYQF SWY +SLPYLL

Sbjct: 311 HFFLTLPSSLSFSDVSASRIITKEHVVTAMFVGNFIVFARSLHYQFYSWYFYSLPYLL 370

Query: 401 YKARLNFIASIIIVYAAHEYCWLVFPATEQSS 431
 ++ +I++ E CW V+P+T SS

Sbjct: 371 WRTPFPTWLRRLIMFLGIELCWNVPSTPSSS 401

FIGURE 8

K. lactis ALG3

TTTGTTTACAAGCTGATACCAACGAACATGAATACACCGGCAGGTTTACT
GAAGATTGGCAAAGCTAACCTTTTACATCCTTTTACCGATGCTGTATTCAG
TGCGATGAGAGTAAACGCAGAACAAATTGCATACATTTTACTTGTTACCA
ATTACATTGGAGTACTATTTGCTCGATCATTACACTACCAATTCCTATCTT
GGTACCATTGGACGTTACCAGTACTATTGAATTGGGCCAATGTTCCGTATC
CGCTATGTGTGCTATGGTACCTAACACATGAGTGGTGCTGGAACAGCTAT
CCGCCAAACGCTACTGCATCCACACTGCTACACGCGTGTAACACATACTG
TTATTGGCTGTATTCTTAAGAGGACCCGCAAACCTCGAAAAGTGGTGATAA
CGAAACAACACACGAGAAAGCTGAG

K. lactis Alg3p

FVYKLIPTNMNTPAGLLKIGKANLLHPFTDAVFSAMRVNAEQIAYILLVTNYI
GVLFARSLHYQFLSWYHWTLPVLLNWANVPYPLCVLWYLTHEWCWNSYPP
NATASTLLHACNTYCYWLYSZEDPQTRKVVITKQHTRKL

FIGURE 9

K. lactis ALG3 BLAST

Score	E		(bits)	Value
Sequences producing significant alignments:				
gi 586444 sp P38179 ALG3 YEAST	Dolichyl-P-Man:Man(5)GlcNAc(...)	125		1e-28
gi 984725 gb AAA75352.1	ORF 1	94		4e-19
gi 16226531 gb AAL16193.1 AF428424.1	At2g47760/F17A22.15 {A...	72		1e-12
gi 25367230 pir B84919	Not56-like protein [imported] - Ara...	72		1e-12
gi 21292031 gb EAA04176.1	agCP3388 [Anopheles gambiae str....	69		2e-11
gi 20892051 ref XP_148657.1	similar to Lethal(2)neighbour ...	65		2e-10

Alignments

S. cerevisiae

Score = 125 bits (314), Expect = 1e-28
 Identities = 60/120 (50%), Positives = 83/120 (69%), Gaps = 1/120 (0%)
 Frame = +3

Query: 66 ANLLHPFT-DAVFSAMRVNAEQIAYILLVTNYIGVLFARSLHYQFLSWYHWTLPVLLNWA 242
 ++L HP +AV +A A+ I ++L+ +N+IGVLF+RSLHYQFLSWYHWTLP+L+ W+
 Sbjct: 332 SSLCHPLRKNVAVLNANP--AKTIPFVLIASNFIGVLFSSRLHYQFLSWYHWTLPILIFWS 389

Query: 243 NVPYPLCVLWYLTHEWCWNSYPPNATASTLLHACNTYCYWLYS*EDPQTRKVVITKQHTR 422
 +P+ + +WY+ HEWCWNSYPPN+ ASTLL A NT L + + V + K H R
 Sbjct: 390 GMPFFVGPIWYVLHEWCWNSYPPNSQASTLLALNTVLLLLLA-LTQLSGSVALAKSHLR 448

A. thaliana

Score = 72.0 bits (175), Expect = 1e-12
 Identities = 42/107 (39%), Positives = 57/107 (53%), Gaps = 3/107 (2%)
 Frame = +3

Query: 84 FTDVAVFSAMRVNAEQIAYILLVTNYIGVLFARSLHYQFLSWYHWTLPVLLNWANVPYPLC 263
 F+D S + + E + + V N+IG++FARSLHYQF SWY ++LP LL P L
 Sbjct: 322 FSDVSASRI-ITKEHVVTAMFVGNGFIGIVFARSLHYQFYSWYFYSLLPYLLWRTPFPTWLR 380

Query: 264 VLWYLTHEWCWNSYPPNATASTL---LHACNTYCYWLYS*EDPQTRK 395
 ++ +L E CWN YP ++S L LH WL DP K
 Sbjct: 381 LIMFLGIELCWNVYPSTPSSSGLLCLHLIILVGLWLAPSVDPYQLK 427

FIGURE 10

S. cerevisiae ALG9

ATGAATTGCAAGGCGGTAACCATTAGTTTATTACTGTTGTTATTTTTAACAAGAGT
 ATATATTCAGCCGACATTCTCGTTAATTTTCAGATTGCGATGAAACCTTTTAATTATT
 GGGAACCATTAAATTTATTGGTACGTGGATTGGTAAACAAACCTGGGAATATTC
 ACCCGAGTATTCTATTAGATCATGGGCTTTCTTATTACCTTTTTACTGTATTCTTTA
 TCCAGTAAACAAATTTACTGACCTAGAAAGTCATTGGAACCTTTTTCATCACAAGA
 GCATGCTTAGGCTTTTTTAGTTTTATCATGGAATTTAAACTACATCGTGAAATTGC
 AGGCAGCTTGGCATTGCAAATCGCAAATATTTGGATTATTTTCCAATTGTTTAATC
 CGGGCTGGTTCCATGCATCTGTGGAATTATTGCCTTCTGCCGTTGCCATGTTGTTG
 TATGTAGGTGCCACCAGACACTCTCTACGCTATCTGTCCACTGGGTCTACTTCTAA
 CTTTACGAAAAGTTTAGCGTACAATTTCTGGCTAGTATACTAGGCTGGCCATTTG
 TTTTAATTTTAAGCTTGCCATTATGTTTACATTACCTTTTCAACCATAGAATTATTT
 CTACCATCAGAACCGCATTTCGACTGCTGTTTGATATTTTCATTGACTGCATTTGCT
 GTGATTGTCACTGACAGTATATTTTACGGGAAGCTTGCTCCTGTATCATGGAACA
 TCTTATTTTACAATGTCATTAATGCAAGTGAGGAATCTGGCCCAAATATTTTCGGG
 GTTGAGCCATGGTACTACTATCCACTAAATTTGTTACTGAATTTCCCACTGCCTGT
 GCTAGTTTTAGCTATTTTGGGAATTTTCCATTTGAGATTATGGCCATTATGGGCAT
 CATTATTCACATGGATTGCCGTTTTCACTCAACAACCTCACAAAGAGGAAAAGATT
 TCTCTATCCAATTTACGGGTTAATAACTTTGAGTGCAAGTATCGCCTTTTACAAAG
 TGTGAATCTATTCAATAGAAAAGCCGATTCTTAAAAAAGGTATAAAGTTGTCAGT
 TTTATTAATTGTTGCAGGCCAGGCAATGTCACGGATAGTGGCTTTGGTGAACAAAT
 TACACAGCTCCTATAGCCGTCTACGAGCAATTTTCTTCACTAAATCAAGGTGGTG
 TGAAGGCACCGGTAGTGAATGTATGTACGGGACGTGAATGGTATCACTTCCCAAG
 TTCTTTCTGCTGCCAGATAATCATAGGCTAAAATTTGTTAAATCTGGATTTGATG
 GTCTTCTTCCAGGTGATTTTCCAGAGAGTGGTTCTATTTTCAAAAAGATTAGAAT
 TTACCTAAGGGAATGAATAACAAGAATATATATGATACCGGTAAAGAGTGGCCG
 ATCACTAGATGTGATTATTTTATTGACATCGTCGCCCAATAAATTTAACAAAAG
 ACGTTTTCAACCCTCTACATCTGATGGATAACTGGAATAAGCTGGCATGTGCTGC
 ATTCATCGACGGTGAAAATTCTAAGATTTTGGGTAGAGCATTTTACGTACCGGAG
 CCAATCAACCGAATCATGCAAATAGTTTTACCAAAAACAATGGAATCAAGTGTACG
 GTGTTGCTTACATTGATTACTGTTTGTGTTGAAAAACCAACTGAGACTACTAATTGA

S. cerevisiae Alg9p

MNCKAVTISLLLLLFLTRVYIQPTFSLISDCDETFNYWEPLNLLVRGFGKQTWEYSPE
 YSIRSWAFLLPFYCILYPVNKFTDLESHWNFFITRACLGFFSFIMEFKLHREIAGSLALQ
 IANIWIIFQLFNPWFHASVELLPASVAMLLYVGATRHSLRYLSTGSTSNFTKSLAYN
 FLASILGWPFVLILSLPLCLHYLFNHRHISTIRTAFCCLIFSLTAFVIVTDSIFYGKLAP
 VSWNILFYNVINASEESGPNIFGVEPWYYPYPLNLLNFPLPVLVLAAILGIFHLRLWPLW
 ASLFTWIAVFTQQPHKEERFLYPIYGLITLSASIAFYKVLNLFNRKPILKKGIKLSVLLI
 VAGQAMSRIVALVNNYTAPIAVVEQFSSLNQGGVKAPVVNVCTGREWYHFPSSFLLP
 DNHRLKFVKSFGDGLLPDGFPESGSIFKKIRTLPGKGMNNKNIYDTGKEWPITRCDYFI
 DIVAPINLTKDVFNPLHLMDNWNKLACAAAFIDGENSKILGRAFYVPEPINRIMQIVLP
 KQWNQVYGVRYIDYCLFEKPTETTN

FIGURE 11

P. pastoris ALG9

TGGCCTTCCTGTCTGCTCGATACTTCCTTTTACAGTAACCAACATACATGTT
CTCCAACATGCTCTTGTATGTATTGGCCTATTCTATCTTGAGACTTGATATC
AACCTTCTATGGTATTATTTTCAGACTGTGATGAAGTGTTCAACTACTGGGA
GCCACTCAACTTCATGCTTAGAGGGTTTGGAAAACAGACTTGGGAGTATT
CTCCAGAGTATGCCATCCGATCTTGGTCCTATCTAGTGCCACTTTGGATAG
CAGGCTATCCACCATTGTTCCCTGGATATCCCTTCTTACTACTTTTTCTACTT
TTTCAGACTACTGCTGGTTATTTTTTTCATTGGTTGCAGAAGTCAAGTTGTA
CCATAGTTTGAAGAAAAATGTCAGCAGTAAGATCAGTTTCTGGTACCTTCT
ATTTACAACCGTTGCTCCAGGAATGTCTCATAGCACGATAGCCTTATTACC
ATCCTCTTTTGCTATGGTTTGTACACTTTTGCCATTAGATACGTCATTGAT
TACCTACAATTACCAACATTAATGCGCACAATCAGAGAGACTGCTGCCAT
CTCACCAGCTCACAAACAACAACACTAGCCAACCTCTCTC

P. pastoris Alg9p

WPSCLLDTSFYSNQHTCSPTCSCMYWPILSZDLISTFYGIISDCDEVFNYWEPL
NFMLRGFGKQTWEYSPEYAIRSWSYLVPLWLAGYPPLFLDIPSYFFFYFFRLLL
VIFSLVAEVKLYHSLKKNVSSKISFWYLLFTTVAPGMSHSTIALLPSSFAMVCH
TFAIRYVIDYLQLPTLMRTIRETAAISPAHKQQLANSL

FIGURE 12 (sheet 1)

P. pastoris ALG9 BLAST

Score	E		(bits)	Value
Sequences producing significant alignments:				
gi 6324110 ref NP_014180.1		catalyzes the transfer of manno...	131	1e-29
gi 21296668 gb EAA08813.1		agCP7810 [Anopheles gambiae str....]	110	2e-23
gi 7019765 emb CAB75773.1		putative mannosyltransferase inv...	104	1e-21
gi 26341066 dbj BAC34195.1		unnamed protein product [Mus mu...	99	4e-20
gi 16551378 gb AAL25798.1		DIBD1 [Homo sapiens]	99	4e-20
gi 19527202 ref NP_598742.1		RIKEN cDNA 8230402H15 [Mus mus...	99	4e-20
gi 12053349 emb CAB66861.1		hypothetical protein [Homo sapi...	99	4e-20

Alignments

S. cerevisiae

Score = 131 bits (329), Expect = 1e-29
 Identities = 62/141 (43%), Positives = 91/141 (64%), Gaps = 1/141 (0%)
 Frame = +2

Query: 200 ISTFYGIISDCDEVFNWYWEPLNFMRLRGFGKQTWEYSPEYAIRSWSYLVPLWIAGYP-PLF 376
 I + +ISDCDE FNYWEPLN ++RGFGKQTWEYSPEY+IRSW++L+P + YP F
 Sbjct: 21 IQPTFSLISDCDETFFNYWEPLNLLVRGFGKQTWEYSPEYSIRSWAFLLPFYICILYPVNKF 80

Query: 377 LDIPSXXXXXXXXRLLLVI FSLVAEVKLYHSLKKNVSSKISFWYLLFTTVAPGMSHSTIAL 556
 D+ S R L FS + E KL+ + +++ +I+ +++F PG H+++ L
 Sbjct: 81 TDLESHWNFFITRACLGFFSFIMEFKLHREIAGSLALQIANIWIIFQLFNPGWFHASVEL 140

Query: 557 LPSSFAMVCHTFAIRYVIDYL 619
 LPS+ AM+ + A R+ + YL
 Sbjct: 141 LPSAVAMLLYVGATRHSRLRYL 161

Anopheles gambiae

Score = 110 bits (274), Expect = 2e-23
 Identities = 58/130 (44%), Positives = 79/130 (60%), Gaps = 3/130 (2%)
 Frame = +2

Query: 197 LISTFYGIISDCDEVFNWYWEPLNFMRLRGFGKQTWEYSPEYAIRSWSYLVPLWIAGYPPLF 376
 L S Y IISDCDE +NYWEPL+++L+G G QTWEYSPE+A+RS+SY LW+ G P
 Sbjct: 34 LQSALYSIISDCDETFFNYWEPLHYLLKGKGFQTWEYSPEFALRSYSY---LWLHGLPAKV 90

Query: 377 LDIPS---XXXXXXXXRLLLVI FSLVAEVKLYHSLKKNVSSKISFWYLLFTTVAPGMSHST 547
 L + + R LL + + E +LY L + ++ +LLF + GM S+
 Sbjct: 91 LQLMTDNGVLIFYFVRCLLAVTCALLEYRLYRILGRKCGGGVASLWLLFQLTSAGMFISS 150

Query: 548 IALLPSSFAM 577
 ALLPSSF+M
 Sbjct: 151 AALLPSSFSM 160

FIGURE 12 (sheet 2)

S. pombe

Score = 104 bits (260), Expect = 1e-21
 Identities = 58/157 (36%), Positives = 85/157 (54%)
 Frame = +2

Query: 197 LISTFYGIISDCDEVFNWYWEPLNFMLRGFGKQTWEYSPEYAIRSWSYLVPLWIAGYPPLF 376
 L S + +I DCDEV+NYWEPL+++L G+G QTWEYSPEYAIRSW Y+ + G+
 Sbjct: 26 LTSASFRVIDDCDEVYNYWEPLHYLLYGYGLQTWEYSPEYAIRSWFYIALHAVPGFLARG 85

Query: 377 LDIPSXXXXXXXXRLLLVIFSLVAEVKLYHSLKKNVSSKISFWYLLFTTVAPGMSHSTIAL 556
 L + R +L FS E L ++ +N + ++ V GM ++ +
 Sbjct: 86 LGLSRLHVFYFIRGVLACFSAFCTNLILAVARNFNRAVALHLTSVLFVNSGMWSASTSF 145

Query: 557 LPSSFAMVCHTFAIRYVIDYLQPTLMRTIRETAAIS 667
 LPSSFAM T A+ L P+ RT++ + I+
 Sbjct: 146 LPSSFAMNMVTLALS---AQLSPPSTKRTVKVVSFIT 179

M. musculus

Score = 99.4 bits (246), Expect = 4e-20
 Identities = 57/143 (39%), Positives = 76/143 (53%), Gaps = 1/143 (0%)
 Frame = +2

Query: 152 SPTSCMYWPILS*DLISTFYGIISDCDEVFNWYWEPLNFMLRGFGKQTWEYSPEYAIRSW 331
 +P S + +LS L + ISDCDE FNYWEP ++++ G G QTWEYSP YAIRS+
 Sbjct: 55 APEGSTAFKCLLSARLCAALLSNISDCDETFNYWEPHYLIYKGKFQTWEYSPVYAIRSY 114

Query: 332 SY-LVPLWIAGYPPLFLDIPSXXXXXXXXRLLLVIFSLVAEVKLYHSLKKNVSSKISFWYL 508
 +Y L+ W A + L R LL S V E+ Y ++ K +S L
 Sbjct: 115 AYLLLHAWPAAFHARILQTNKILVFYFLRCLLAFVSCVCELYFYKAVCKKFGHLVSRMML 174

Query: 509 LFTTVAPGMSHSTIALLPSSFAM 577
 F ++ GM S+ A LPSSF M
 Sbjct: 175 AFLVLSTGMFCSSSAFLPSSFCM 197

H. sapiens

Score = 99.4 bits (246), Expect = 4e-20
 Identities = 56/143 (39%), Positives = 76/143 (53%), Gaps = 1/143 (0%)
 Frame = +2

Query: 152 SPTSCMYWPILS*DLISTFYGIISDCDEVFNWYWEPLNFMLRGFGKQTWEYSPEYAIRSW 331
 +P S + +LS L + ISDCDE FNYWEP ++++ G G QTWEYSP YAIRS+
 Sbjct: 55 APEGSTAFKCLLSARLCAALLSNISDCDETFNYWEPHYLIYGEGFQTWEYSPAYAIRSY 114

Query: 332 SY-LVPLWIAGYPPLFLDIPSXXXXXXXXRLLLVIFSLVAEVKLYHSLKKNVSSKISFWYL 508
 +Y L+ W A + L R LL S + E+ Y ++ K +S L
 Sbjct: 115 AYLLLHAWPAAFHARILQTNKILVFYFLRCLLAFVSCICELYFYKAVCKKFGHLVSRMML 174

Query: 509 LFTTVAPGMSHSTIALLPSSFAM 577
 F ++ GM S+ A LPSSF M
 Sbjct: 175 AFLVLSTGMFCSSSAFLPSSFCM 197

FIGURE 13

S. cerevisiae ALG12

ATGCGTTGGTCTGTCCTTGATACAGTGCTATTGACCGTGATTTTCCTTTCATCTAAT
 CCAAGCTCCATTACCAAGGTGGAAGAGAGTTTTAATATTCAAGCCATTCATGAT
 ATTTTAACCTACAGCGTATTTGATATCTCCCAATATGACCACTTGAAATTTCTGG
 AGTAGTCCCTAGAACATTCGTTGGTGCTGTGATTATTGCAATGCTTTCGAGACCTT
 ATCTTTACTTGAGTTCTTTGATCCAACTTCCAGGCCTACGTCTATAGATGTTCAA
 TTGGTCGTTAGGGGGATTGTTGGCCTACCAATGGGCTTTCTTTTATCTATTTAAA
 GAATTGTTTGCAAGATATGTTTGATGAAATCACTGAAAAGAAAAAGGAAGAAAA
 TGAAGACAAGGATATATACATTTACGATAGCGCTGGTACATGGTTTCTTTTATTTT
 TAATTGGCAGTTTCCACCTCATGTTCTACAGCACTAGGACTCTGCCTAATTTTGTC
 ATGACTCTGCCTCTAACCAACGTCGCATTGGGGTGGGTTTTATTGGGTCGTTATAA
 TGCAGCTATATTCCTATCTGCGCTCGTGGCAATTGTATTTAGACTGGAAGTGTCAG
 CTCTCAGTGCTGGTATTGCTCTATTTAGCGTCATCTTCAAGAAGATTTCTTTATTC
 GATGCTATCAAATTCGGTATCTTTGGCTTGGGACTTGGTTCGCCATCAGTATCAC
 CGTTGATTATATTTCTGGCAAGAATGGTGTCTACCTGAGGTAGATGGTTTCTTGT
 TCAACGTGGTTGCGGGTTACGCTTCCAAGTGGGGTGTGGAGCCAGTTACTGCTTA
 TTTCACGCATTACTTGAGAATGATGTTTATGCCACCAACTGTTTTACTATTGAATT
 ACTTCGGCTATAAATTAGCACCTGCAAAATTAATAAATTGTCTCACTAGCATCTCTT
 TTCCACATTATCGTCTTATCCTTTCAACCTCACAAGAATGGAGATTCATCATCTA
 CGCTGTTCCATCTATCATGTTGCTAGGTGCCACAGGAGCAGCACATCTATGGGAG
 AATATGAAAGTAAAAAAGATTACCAATGTTTTATGTTTGGCTATATTGCCCTTATC
 TATAATGACCTCCTTTTTTCATTTCAATGGCGTTCTTGTATATATCAAGAATGAATT
 ATCCAGGCGGCGAGGCTTTAACTTCTTTTAATGACATGATTGTGGAAAAAATAT
 TACAAACGCTACAGTTCATATCAGCATACCTCCTTGCATGACAGGTGTCATTTTAT
 TTGGTGAATTGAACTACGGTGTGTACGGCATCAATTACGATAAGACTGAAAATAC
 GACTTTACTGCAGGAAATGTGGCCCTCCTTTGATTTCTTGATCACCCACGAGCCA
 ACCGCCTCTCAATTGCCATTGAGAATAAGACTACCAACCATTGGGAGCTAGTTA
 ACACAACAAAGATGTTTACTGGATTTGACCCAACCTACATTAAGAACTTTGTTTT
 CCAAGAGAGAGTGAATGTTTTGTCTCTACTCAAACAGATCATTTTCGACAAGACC
 CCTACCGTTTTTTTTGAAAGAATTGACGGCCAATTCGATTGTTAAAAGCGATGTCTT
 CTTACCTATAAGAGAATCAAACAAGATGAAAAAACTGATTGA

S. cerevisiae Alg12p

MRWSVLDTVLLTVISFHLIQAPFTKVEESFNIQAIHDILTYSVFDISQYDHLKFPGVVP
 RTFVGAVIAMLSPYLYLSSLIQTSRPTSIDVQLVVRGIVGLTNGLSFIYLNCLQDM
 FDEITEKKKEENEDKDIYIYDSAGTWFLFLIGSFHLMFYSTRTLPNFVMTLPLTNVAL
 GWVLLGRYNAAIFLSALVAIVFRLEVSALSAGIALFSVIFKKISLFDKIFGIFGLGLGS
 AISITVDSYFWQEWCLPEVDGFLFNVAAGYASKWGVPEPVTAYFTHYLRMMFMPPTV
 LLLNYFGYKLAPAKLKIVSLASLFHIIVLSFQPHKEWRFIYAVPSIMLLGATGAHLW
 ENMKVKKITNVLCAILPLSIMTSFFISMAFLYISRMNYPGGEALTSFNDMIVEKNITN
 ATVHISIPPCMTGVTLFGELNYGVYGINYDKTENTLLQEMWPSFDFLITHEPTASQLP
 FENKTTNHVELVNTTKMFTGFDPTYIKNFVFQERVNVLSLLKQIIFDKTPTVFLKELT
 ANSIVKSDVFFTYKRIKQDEKTD

FIGURE 14

P. pastoris ALG12

TCGGTCGAGAATGATAACTGAAGAACTCAAAATCTCTCACACTTTTCATCGT
TACTGTACTGGCAATCATTGCATTTTCAGCCTCATAAAGAATGGAGATTTAT
AGTTTACATTGTTCCACCACTTGTCATCACCATATCTACAGTACTTGCACA
ACTACCCAGGAGATTCACAATCGTCAAAGTTGCTGTTTTTCTCCTAAGTTT
CGGCTCTTTGCTCATATCCCTGTCGTTTCTTTTCATCTCATCGTATAACTAC
CCTGGGGGGTGAAGCTTTACAGCATTGGAACGAGAACTCCTTCTACTGGA
CCAAAGTTCCCTACCTGTTGATATTAAGGTTTCATATGGATGTCCCTGCATG
CATGACTGGGGTGACTTTATTTGGTTACTTGGATAACTCAAAATTGAACAA
TTTAAGAATTGTCTATGATAAAACAGAAGACGAGTCGCTGGACACAATCT
GGGATTCTTTCAATTATGTCATCTCCGAAATTGACTTGGATTCTTCGACTG
CTCCCAAATGGGAGGGGGGATTGGCTGAAGATTGATGTTGTCCAAGGCTAC
AACGGCATCAATAACAATCTATCAAAAATACAATTTTCAATTATGGAAT
ACTTAAACGGATGATAAGAGACGCAACCAAACCTTGATGTTGGATTTATTC
GTACGGTCTTTTCGATCCTTCATAAAATTTGATGATAAATTATTCATTTATG
AGAGGAGCAGTCAAACCTGAAAATATATACCTCATTTGTTCAATTTGGTGT
AAAGAGTGTGGCGGATAGACTTCTTGTAATCAGGAAAGCTACAATTCCA
ATTGCTGCAAAAATACCAATGCCCATAA

P. pastoris Alg12p

RMITEELKISHTFIVTVLAIIAFQPHKEWRFIVYIVPPLVITISTVLAQLPRRFTIV
KVAVFLLSFGSLLISLSFLFISSYNYPGGEALQHLNEKLLLLDQSSLPVDIKVH
MDVPACMTGVTLFGYLDNSKLNLRIVYDKTEDESLDTIWDSFNYSVISEIDL
SSTAPKWECDWLKIDVVQGYNGINKQSIKNTIFNYGILKRMIRDATKLDVGF
RTVFRSFIKFDDKLFYIERSSQ

FIGURE 15 (sheet 1)

P. pastoris ALG12 BLAST

Sequences producing significant alignments:			Score	E
			(bits)	Value
gi 1302525 emb CAA96310.1	ORF YNR030w [Saccharomyces cerev...	102	5e-21	
gi 19112221 ref NP_595429.1	putative involvement in cell w...	56	5e-07	
gi 15864569 emb CAC83681.1	putative dolichyl-p-man: Man7G1...	53	4e-06	
gi 13129114 ref NP_077010.1	dolichyl-p-mannose:Man7GlcNAc2...	53	4e-06	
gi 22266724 gb AAM94900.1 AF311904.1	membrane protein SB87 ...	53	4e-06	
gi 18478284 emb CAD22101.1	putative mannosyltransferase [M...	52	8e-06	

Alignments

S. cerevisiae

Score = 102 bits (255), Expect = 5e-21
 Identities = 74/258 (28%), Positives = 121/258 (46%), Gaps = 19/258 (7%)

Query: 8 RMITEELKISHTFIVTVLAIIAFQPHKEWRFIVYIVPPLVITISTVLAQLPRRFTIVKVA 187
 ++ +LKI + + +++FQPHKEWRFI+Y VP +++ +T A L + K+
 Sbjct: 302 KLAPAKLKIVSLASLFHIIIVLSFQPHKEWRFIIYAVPSIMLLGATGAHLWENMKVKKIT 361

Query: 188 -----VXXXXXXXXXXXXXXXXXXNYPGGEALQHLNEKLLLLDQSSLPVDIKVHMD 346
 + NYPGGEAL N+ ++ + VH+
 Sbjct: 362 NVLCLAILPLSIMTSFFISMAFLYISRMNYPGGEALTSFNDMIV----EKNITNATVHIS 417

Query: 347 VPACMTGVTLFGYLDNSKLNLRIVYDKTEDES-LDTIWDSFNYVI-----SEIDLSS 505
 +P CMTGVTLFG L+ I YDKTE+ + L +W SF+++I S++ ++
 Sbjct: 418 IPPCMTGVTLFGELNYGVYG---INYDKTENTTLLQEMWPSFDLITHEPTASQLPFENK 474

Query: 506 TAPKWECDWLKIDVVQGYNGINKQSIKNTIFN-----YGILKRMIRDATKLDVGFIRTVF 670
 T WE ++ + + G + IKN +F +LK++I D K F++ +
 Sbjct: 475 TTNHWE----LVNTTKMFTGFDPTYIKNFVFQERVNVLSSLKQIIFD--KTPTVFLKELT 528

Query: 671 RSFIKFDKLFYIERSSQ 724
 + I D F Y+R Q
 Sbjct: 529 ANSIVKSDVFFTYKRIKQ 546

S. pombe

Score = 56.2 bits (134), Expect = 5e-07
 Identities = 46/152 (30%), Positives = 62/152 (40%), Gaps = 11/152 (7%)

Query: 65 IIAFQPHKEWRFIVYIVPPLVITISTVLAQL-----PRRFTIVKVAVXXXXXXXXXX 220
 + +F HKEWRFI+Y + P S + A L + F I+++
 Sbjct: 295 VYSFLGHKEWRFIIYSI-PWFNAASAIGASLCFNASKFGKKIFEILRLMFFSGIIFGFIG 353

Query: 221 XXXXXXXXXXXNYPGGEALQHLNEKLLLLDQSSLPVDIKVHMDVPACMTGVTLFGYLDNSK 400
 Y YPGG AL L E + VHMDV CMTG+T F L +
 Sbjct: 354 SSFLLYVFQYAYPGGLALTRLYE-----IENHPQVSVHMDVYPCMTGITRFSQLPS-- 404

FIGURE 15 (sheet 2)

Query: 401 LNNLRIVYDKTEDESL---DTIWDSFNYVISE 487
 YDKTED + F+Y+I+E
 Sbjct: 405 -----WYYDKTEDPKMLSNSLFISQFDYLITE 431

Homo sapiens

Score = 53.1 bits (126), Expect = 4e-06
 Identities = 41/149 (27%), Positives = 68/149 (45%), Gaps = 6/149 (4%)

Query: 59 LAIIAFQPHKEWRFIVYIVPPLVITISTVLAQLPRR-----FTIVKVAVXXXXXXXXXX 220
 +A+ + PHKE RFI+Y P L IT + + L + + V

Sbjct: 299 MALYSLLPHKELRFIIYAFPMLNITAARGCSYLLNNYKKSPLYKAGSLLVIGHLVVNAAY 358

Query: 221 XXXXXXXXXYNYPGGEALQHLNEKLLLLDQSSLPVDIKVHMDVPACMTGVTLEFGYLDNSK 400
 +NYPGG A+Q L++ L+ Q+ D+ +H+DV A TGV+ F ++++

Sbjct: 359 SATALYVSHFNYPGGVAMQRLHQ--LVPPQT---DVLLHIDVAAAQTGVSRLQVNSAW 412

Query: 401 LNNLRIVYDKTEDESLDTIWDSFNYVISE 487
 YDK ED T ++ +++ E

Sbjct: 413 R-----YDKREDVQPGTGMLAYTHILME 435

Applied Biosystems Voyager System 6235

Voyager Spec #1[BP = 1463.3, 2852]

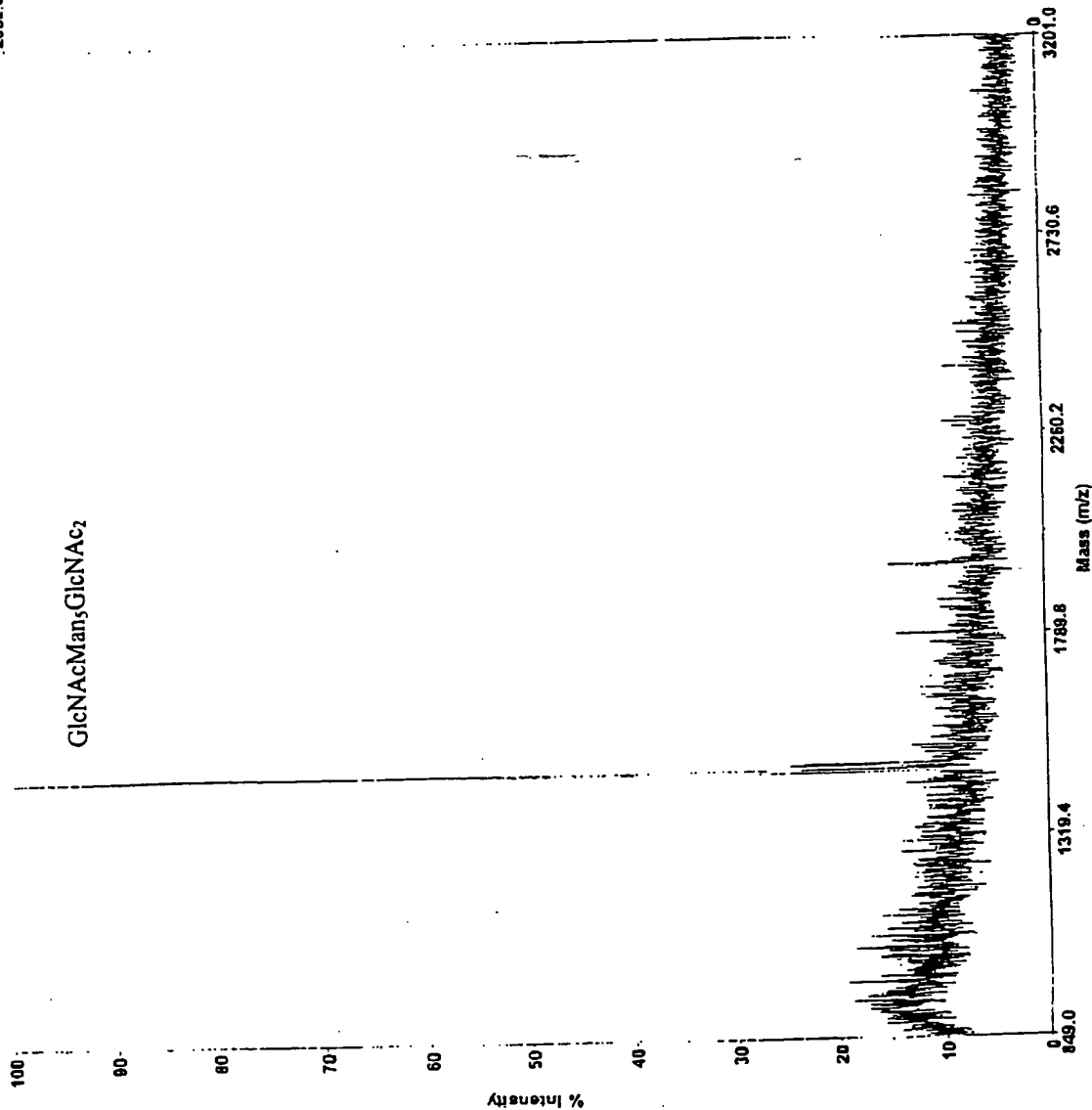


FIGURE 16

Mode of operation: Linear
Extraction mode: Delayed
Polarity: Positive
Acquisition control: Manual
2852.0 Acquisition control: Manual

Accelerating voltage: 20000 V
Grid voltage: 93%
Guide wire U: 0.1%
Extraction delay time: 125 nsec

Acquisition mass range: 850 -- 3200 Da
Number of laser shots: 200/spectrum
Laser intensity: 2786
Laser Rep Rate: 20.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxydynamac ac
Low mass gate: 800 Da

Digitizer start time: 19.955
Bin size: 0.5 nsec
Number of data points: 37310
Vertical scale: 500 mV
Vertical offset: 0%
Input bandwidth: 500 MHz

Sample well: 22
Plate ID: 100 WELL PLATE
Serial number: 6235
Instrument name: Voyager-DE PRO
Plate type filename: C:\VOYAGER\100 well plate.pl
Lab name: PE Biosystems

Absolute x-position: 6212.96
Absolute y-position: 35933.8
Relative x-position: -454.524
Relative y-position: -1213.7
Shots in spectrum: 200
Source pressure: 6.934e-007
Mirror pressure: 8.818e-008
TC2 pressure: 0.01188
TIS gate width: 10
TIS flight length: 669

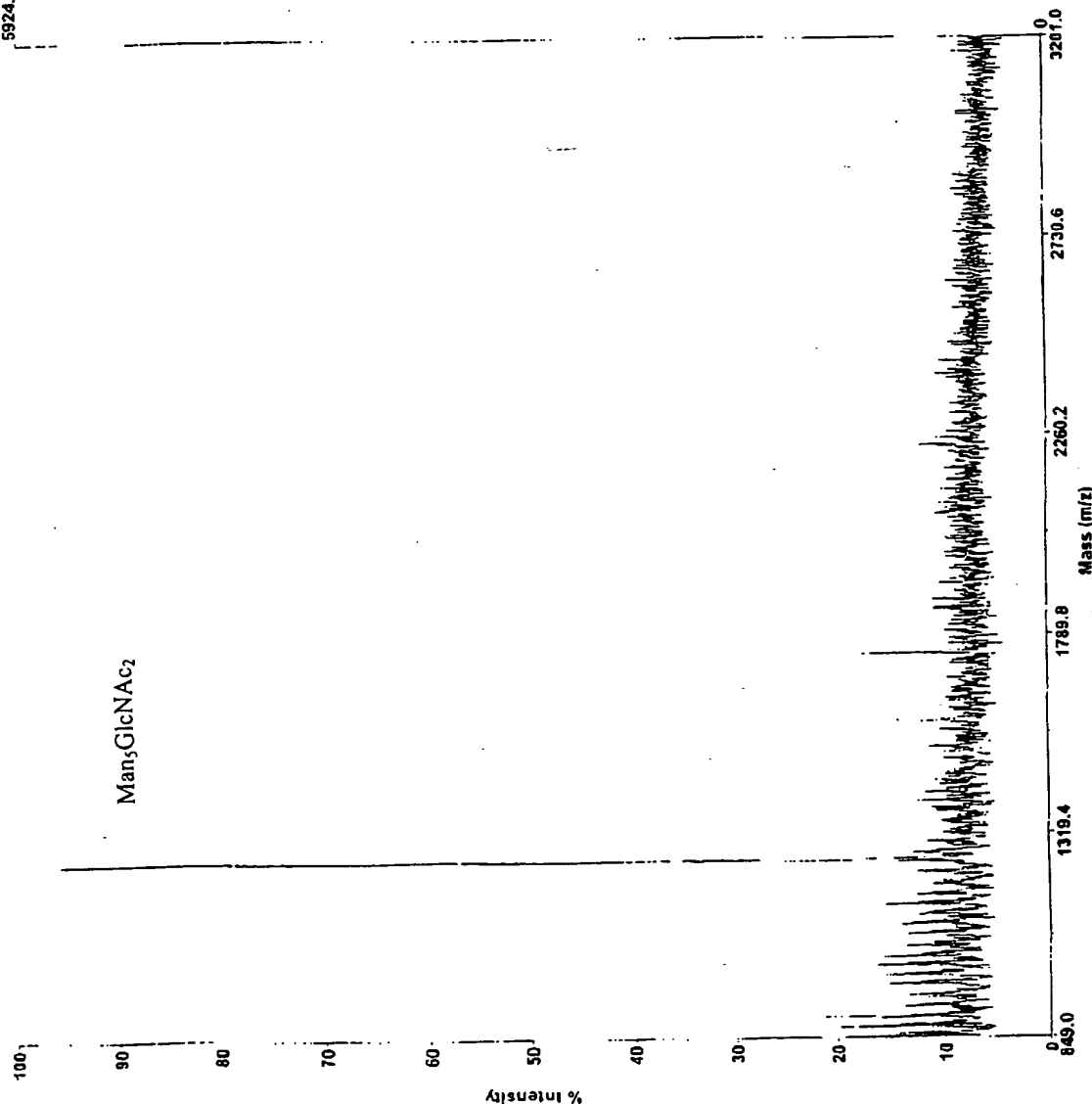
Printed: 10:47, December 18, 200

Acquired: 11:42:00, November 08, 2002

Applied Biosystems Voyager System 6235

Voyager Spec #1[BP = 1259.4, 5924]

FIGURE 17



Mode of operation: Linear
Extraction mode: Delayed
Polarity: Positive
Acquisition control: Manual
5924.0
Accelerating voltage: 20000 V
Grid voltage: 93%
Guide wire 0: 0.1%
Extraction delay time: 125 nsec
Acquisition mass range: 850 -- 3200 Da
Number of laser shots: 200/spectrum
Laser intensity: 2986
Laser Rep Rate: 20.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxycinnamic a
Low mass gate: 800 Da
Digitizer start time: 19.955
Bin size: 0.5 nsec
Number of data points: 37310
Vertical scale: 500 mV
Vertical offset: 0%
Input bandwidth: 500 MHz
Sample well: 32
Plate ID: 100 WELL PLATE
Serial number: 6235
Instrument name: Voyager-DE PRO
Plate type filename: C:\VOYAGER\100 well plate.p
Lab name: PE Biosystems
Absolute x-position: 6813.36
Absolute y-position: 30808.1
Relative x-position: -54.1439
Relative y-position: -1261.39
Shots in spectrum: 200
Source pressure: 7.708e-007
Mirror pressure: 9.387e-008
TC2 pressure: 0.01262
TIS gate width: 10
TIS light length: 689

Printed: 10:47, December 18, 2000

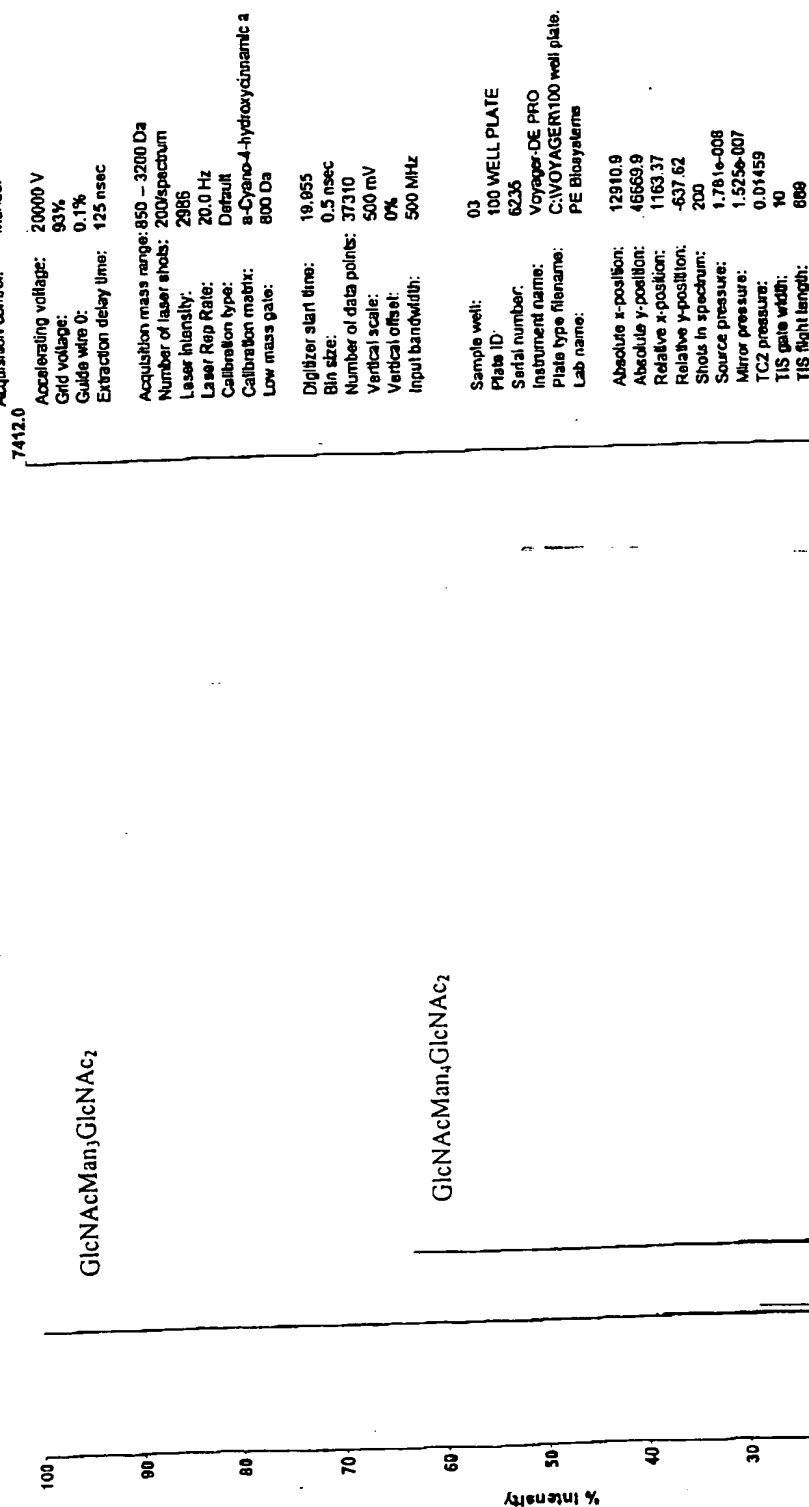
Acquired: 11:30:00, November 08, 2002

D:\Print\multispec\Specs for him\A\Mar 2002\11.8.02\A.M. 1A.21.07 N\127 hour final.mz 0007.dat

Applied Biosystems voyager system

Voyager Spec #1[BP = 1137.8, 7412]

FIGURE 18



Printed: 11:47, December 17, 2002

Acquired: 10:16:00, October 13, 2002

D:\Data\Hujian\Data for burn\Other samples\IOCT 2002\10-13-02\Rob-3_0002.dat

Applied Biosystems Voyager System 6235

Voyager Spec #1[BP = 1139.5, 4716]

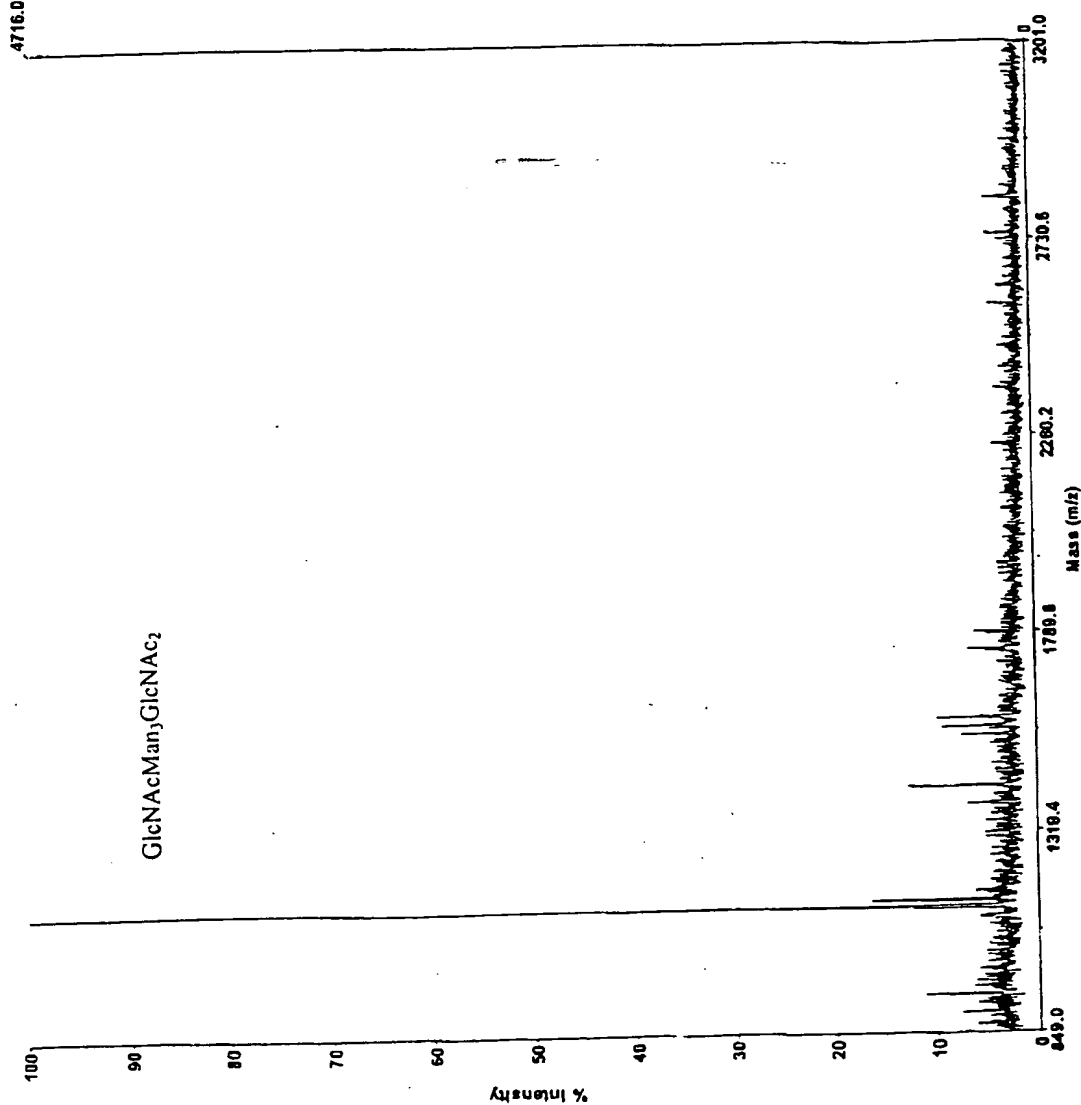


FIGURE 19

Mode of operation: Linear
Extraction mode: Delayed
Polarity: Positive
Acquisition control: Manual
Accelerating voltage: 20000 V
Grid voltage: 93%
Guide wire 0: 0.1%
Extraction delay time: 125 nsec
Acquisition mass range: 850 - 3200 Da
Number of laser shots: 200/spectrum
Laser intensity: 2766
Laser Rep Rate: 20.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxynaphthamic
Low mass gate: 800 Da
Digitizer start time: 19.955
Bin size: 0.5 nsec
Number of data points: 37310
Vertical scale: 500 mV
Vertical offset: 0%
Input bandwidth: 500 MHz
Sample well: 24
Plate ID: 100 WELL PLATE
Serial number: 6235
Instrument name: Voyager-DE PRO
Plate type filename: C:\VOYAGER\100 well plate.j
Lab name: PE Biosystems
Absolute x-position: 18177.2
Absolute y-position: 37530.3
Relative x-position: 1349.67
Relative y-position: 382.81
Shots in spectrum: 200
Source pressure: 1.399e-006
Mirror pressure: 1.235e-007
TC2 pressure: 0.01248
TIS gate width: 10
TIS flight length: 689

Printed: 12:15, December 17, 2001

Acquired: 15:39:00, October 15, 2002

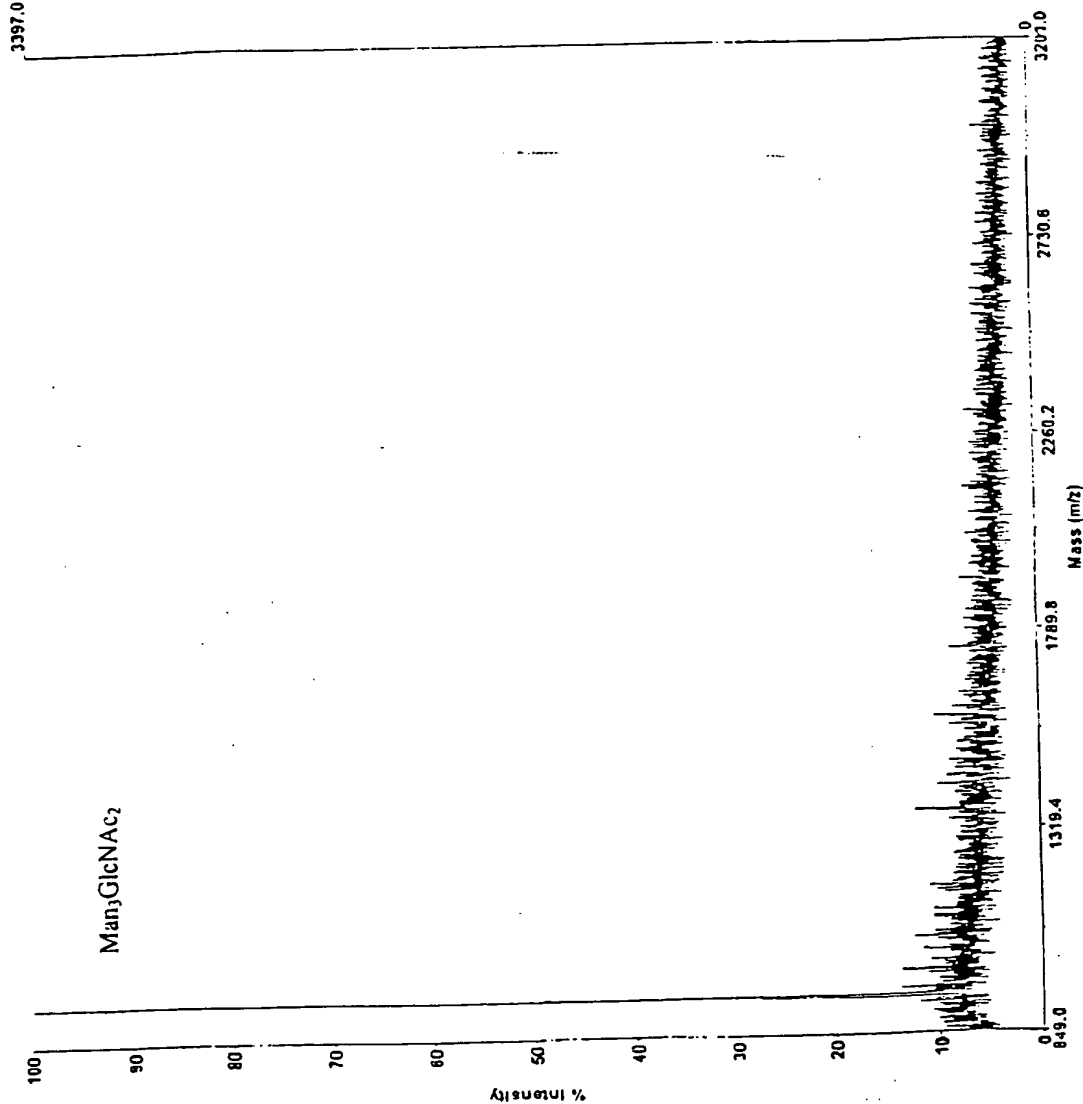
D:\Data\HuanData for burn\Other samples\OCT 2002\10-15-02\6D 10-10-02 3 1.2\digest_0004.dai

Applied Biosystems Voyager System 6235

Voyager Spec #1[BP = 935.7, 3397]

FIGURE 20

Mode of operation: Linear
Extraction mode: Delayed
Polarity: Positive
Acquisition control: Manual
Accelerating voltage: 20000 V
Grid voltage: 93%
Guide wire U: 0.1%
Extraction delay time: 125 nsec
Acquisition mass range: 850 - 3200 Da
Number of laser shots: 200/spectrum
Laser intensity: 2600
Laser Rep Rate: 20.0 Hz
Calibration type: Default
Calibration matrix: a-Cyano-4-hydroxymethyl
Low mass gate: 800 Da
Digitizer start time: 19.955
Pin size: 0.5 nsec
Number of data points: 37310
Vertical scale: 500 mv
Vertical offset: 0%
Input bandwidth: 500 MHz
Sample well: 22
Plate ID: 100 WELL PLATE
Serial number: 6235
Instrument name: Voyager DE PRO
Plate type filename: C:\VOYAGER\100 well plate.t
Lab name: PE Biosystems
Absolute x-position: 5518.88
Absolute y-position: 37692.8
Relative x-position: -1148.62
Relative y-position: 545.303
Shots in spectrum: 200
Source pressure: 6.934e-007
Mirror pressure: 8.466e-008
TCZ pressure: 0.01269
TIS gate width: 10
TIS flight length: 689



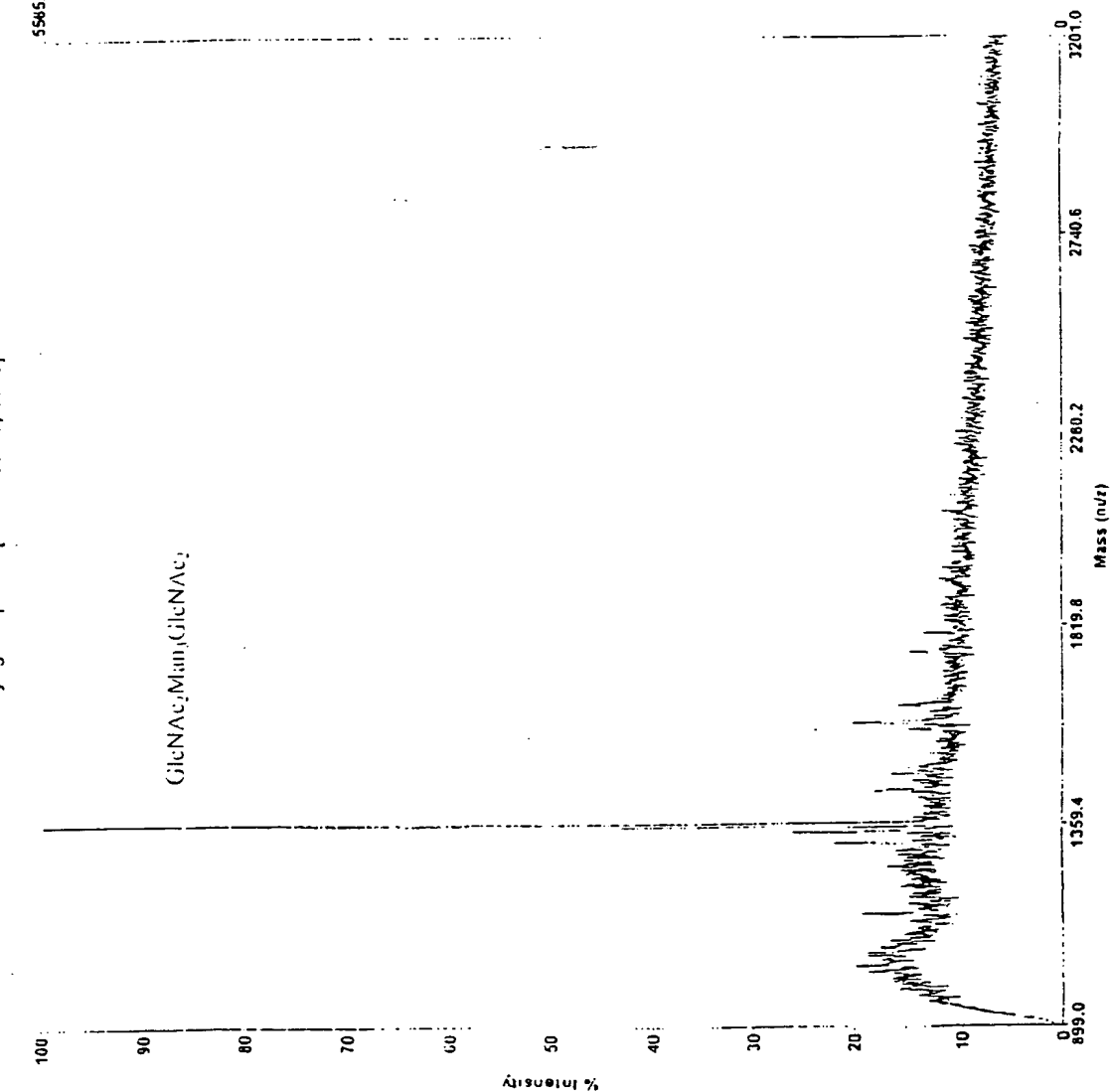
Printed: 12:05, December 17, 2002

Acquired: 14:31:00, November 27, 2002

D:\Data\Hull\anData for burn\Other samples\WV02111-26-02\TH 11-20-02 ROP-27 hexo +1,2 hexosidase_0001.dat

Applied Biosystems Voyager System 6235

Voyager Spec #1[BP = 1356.8, 5565]



Mode of operation: Linear
Extraction mode: Delayed
Polarity: Positive
Acquisition control: Automatic

FIGURE 21

5565.2

Accelerating voltage: 20000 V
Grid voltage: 93%
Guide wire Q: 0.1%
Extraction delay time: 125 msec

Acquisition mass range: 900 - 3200 Da
Number of laser shots: 100/spectrum
Laser intensity: 2882
Laser Rep Rate: 20.0 Hz
Calibration type: Default
Calibration matrix: 3-Cyano-4-hydroxycinnamic acid
Low mass gate: 875 Da

Digital start time: 20.5305
On size: 0.5 msec
Number of data points: 36159
Vertical scale: 500 mV
Vertical offset: 0%
Input transducer: SMI-MHz

Laser control: Manual
Sample positioning: Automated
Random Pattern: Edge Based
Auto storage mode: Accumulate all passing

Min intensity: 226
Max intensity: 0
Resolution: 0
Signal-to-noise: 3

Sample well: 91
Plate ID: 100 WELL PLATE
Serial number: 6235
Instrument name: Voyager-DE PRO
Plate type filename: C:\VOYAGER\100 well plate.p
Lab name: PE Biosystems

Absolute x-position: 1190.1
Absolute y-position: 2397.25
Relative x-position: -397.403
Relative y-position: 809.751
Shots in spectrum: 560
Source pressure: 9.936e-007
Mirror pressure: 9.246e-008
TCZ pressure: 0.0122
TIS gate width: 10
TIS flight length: 609

Printed: 10/59, December 19, 2000

Acquired: 12:57:00, October 28, 2002

Sample Description: Comments:

D:\Data\Huijuan\Data for burn\Screen data\October 2002\UN Media digest 10-23-02 WFB-JN LA 30-32 IV 10-24-02 91_0001.dai

Applied Biosystems Voyager System 6235

Voyager Spec #1 [BP = 934.5, 7357]

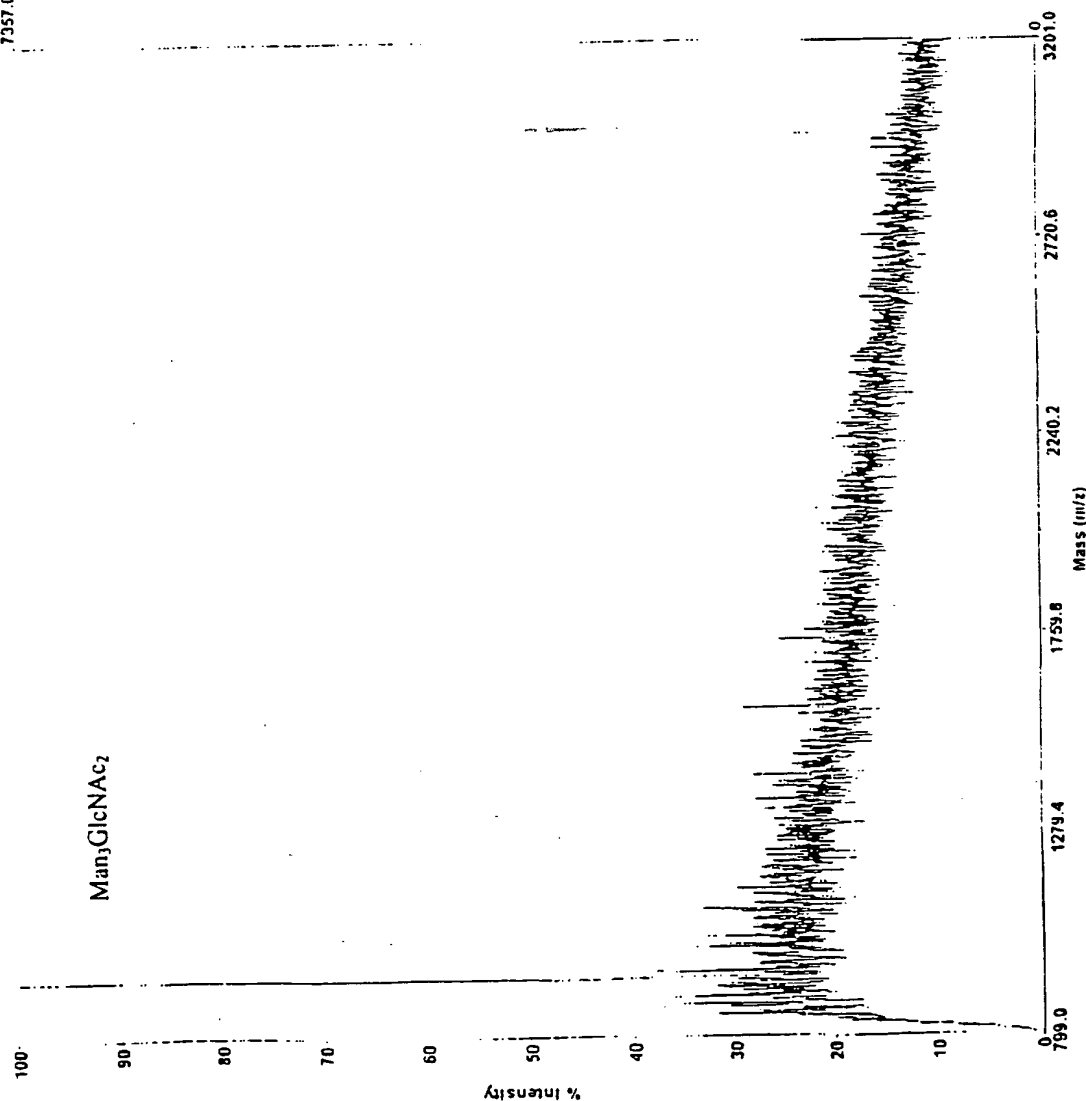


FIGURE 22

Mode of operation:	Linear
Extraction mode:	Delayed
Polarity:	Positive
Acquisition control:	Manual
Accelerating voltage:	19000 V
Grid voltage:	94%
Guide wire D:	0.15%
Extraction delay time:	175 nsec
Acquisition mass range:	800 -- 3200 Da
Number of laser shots:	150/spectrum
Laser intensity:	3052
Laser Rep Rate:	20.0 Hz
Calibration type:	Default
Calibration matrix:	a-Cyano-4-hydroxycinnamic a
Low mass gate:	800 Da
Digitizer start time:	19.8845
Bin size:	0.5 msec
Number of data points:	39555
Vertical scale:	500 mV
Vertical offset:	0%
Input bandwidth:	500 MHz
Sample well:	91
Plate ID:	100 WELL PLATE
Serial number:	0235
Instrument name:	Voyager-DE PRO
Plate type filename:	C:\VOYAGER\100 well plate.p
Lab name:	PE Biosystems
Absolute x-position:	1843.77
Absolute y-position:	306.377
Relative x-position:	256.268
Relative y-position:	-1281.12
Shots in spectrum:	150
Source pressure:	8.071e-007
Minor pressure:	8.165e-008
TC2 pressure:	0.01199
TIS gate width:	10
TIS flight length:	689

Printed: 10:59, December 18, 2000

Acquired: 08:30:00, October 30, 2002

D:\Data\Hulian\Data for burn\Screen data\October 2002\PB-JN LA 30-32 10-24-02 IV\PB-JN LA 30-32 10-24-02 911flexo digest_0007.dat

Applied Biosystems Voyager System 6235

Voyager Spec #1[BP = 1666.9, 3309]

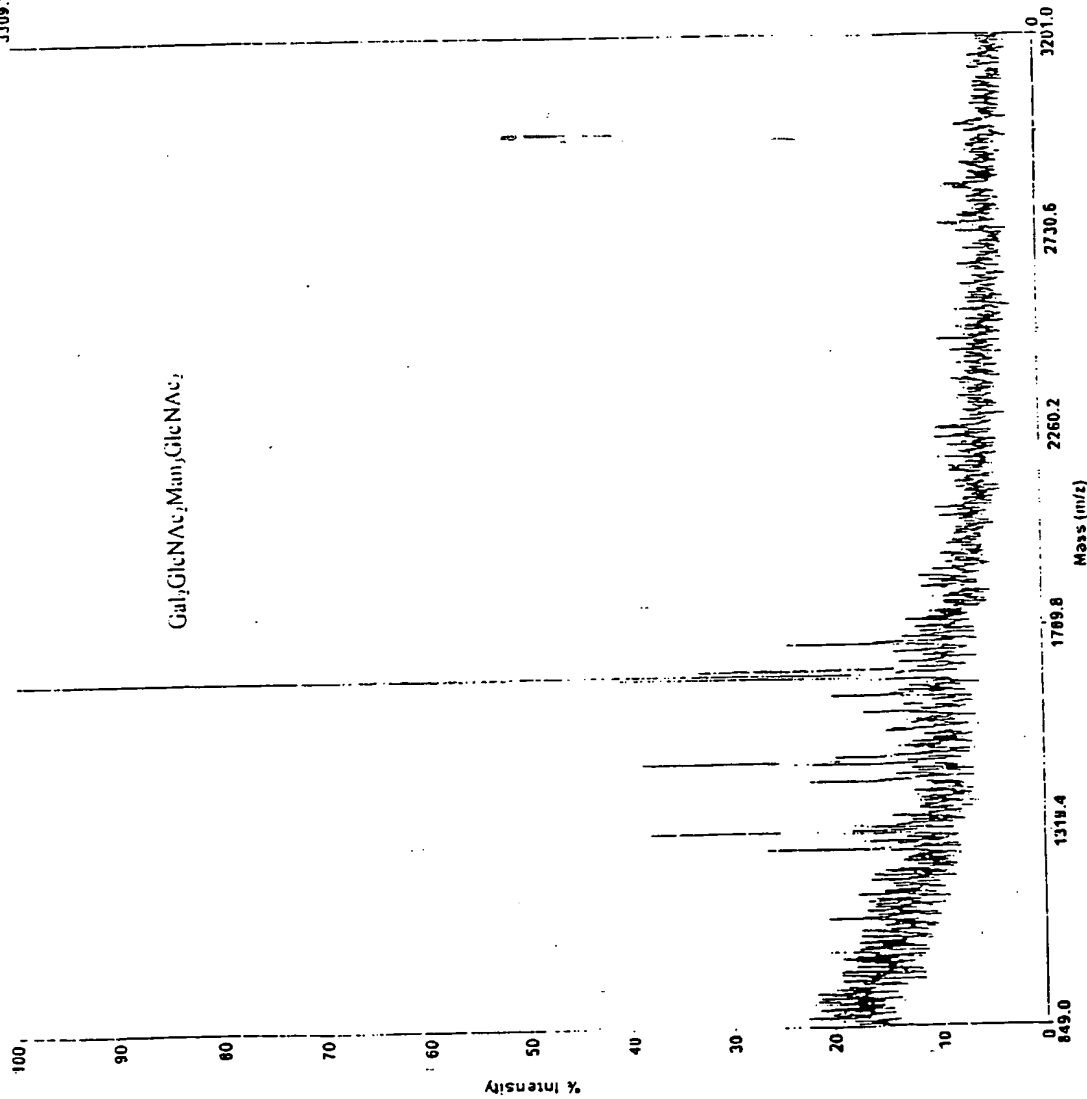


FIGURE 23

Mode of operation: Linear
Extraction mode: Delayed
Polarity: Positive
Acquisition control: Manual
3309.1
Accelerating voltage: 20000 V
Grid voltage: 50%
Guide wire U: 0.1%
Extraction delay time: 125 msec
Acquisition mass range: 850 - 3200 Da
Number of laser shots: 2000/spectrum
Laser intensity: 2000
Laser Rep Rate: 20.0 Hz
Calibration type: Default
Calibration media: a-Cyano-4-hydroxycinnamic acid
Low mass gate: 800 Da
Digitizer start time: 19.955
Ion size: 0.5 msec
Number of data points: 37310
Vertical scale: 500 mV
Vertical offset: 0%
Input bandwidth: 500 MHz
Sample well: 77
Plate ID: 100 WELL PLATE
Serial number: 0235
Instrument name: Voyager-UE PRO
Plate type filename: C:\VOYAGER\100 well plate.p
Lab name: PE Biosystems
Absolute x position: 3.8113 1
Absolute y position: 1.2244 9
Relative x position: 945.594
Relative y position: 513.403
Shots in spectrum: 200
Source pressure: 5.864e-007
Mirror pressure: 7.263e-008
TC2 pressure: 0.01159
TIS gate width: 10
TIS light length: 689

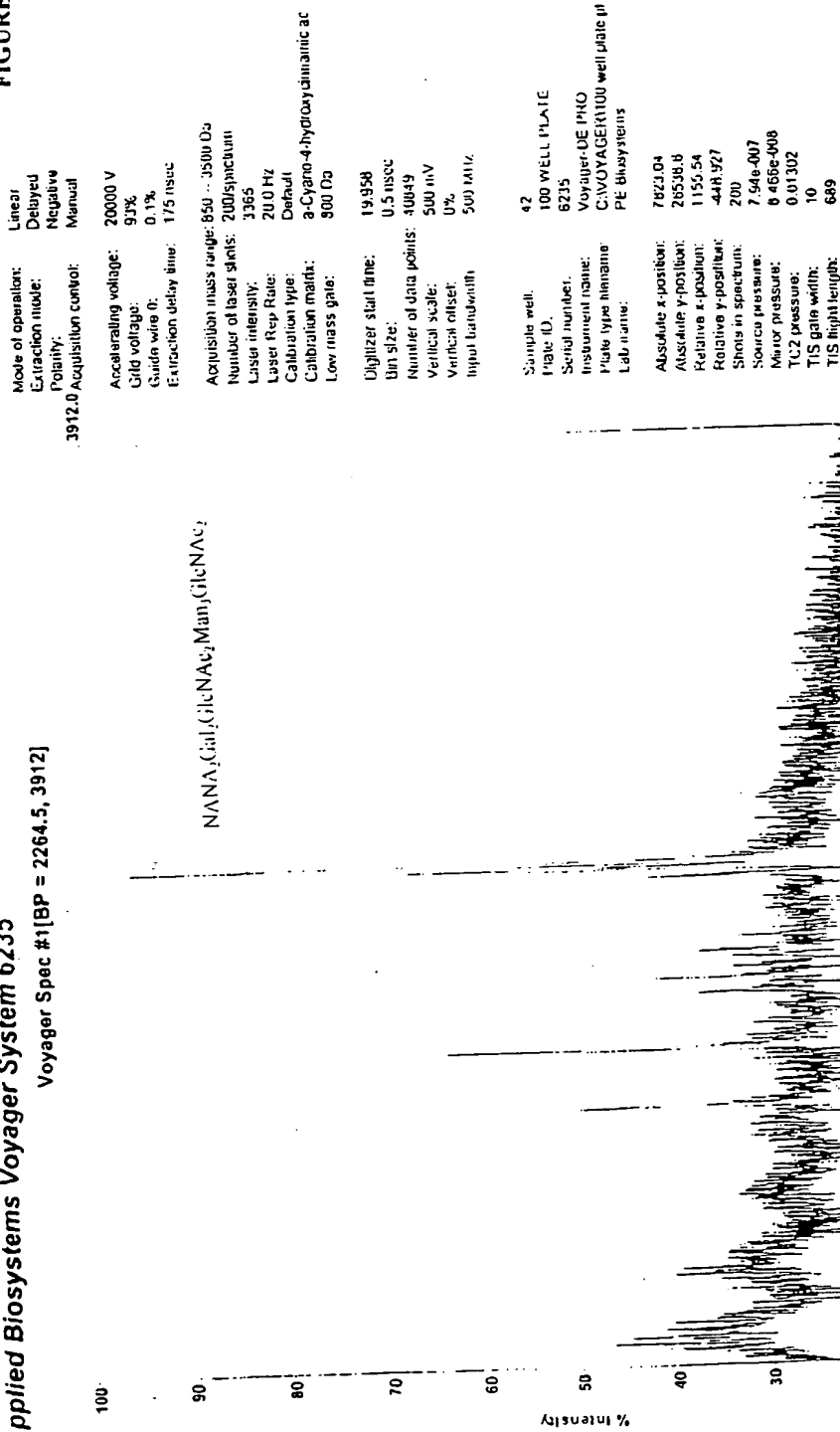
Printed: 11:02, December 19, 2002

Acquired: 13:05:00, December 07, 2002

C:\Instruments\Voyager\100 well plate.p

FIGURE 24

Applied Biosystems Voyager System 6235
Voyager Spec #1[BP = 2264.5, 3912]



Printed: 11/03, December 18, 2002

Acquired: 08:47:00, December 16, 2002
D:\Data\Bios\BP8PC2 c sialtrans_0001.dat

FIGURE 25

S. cerevisiae ALG6

ATGGCCATTGGCAAAAGGTTACTGGTGAACAAACCAGCAGAAGAATCATT
 TTATGCTTCTCCAATGTATGATTTTTTGTATCCGTTTAGGCCAGTGGGGAA
 CCAATGGCTGCCAGAATATATTATCTTTGTATGTGCTGTAATACTGAGGTG
 CACAATTGGACTTGGTCCATATTCTGGGAAAGGCAGTCCACCGCTGTACG
 GCGATTTTGAGGCTCAGAGACATTGGATGGAAATTACGCAACATTTACCG
 CTTTCTAAGTGGTACTGGTATGATTTGCAATACTGGGGATTGGACTATCCA
 CCATTAACAGCATTTCATTTCGTACCTTCTGGGCCTAATTGGATCTTTTTTCA
 ATCCATCTTGGTTTGCCTAGAAAAGTCACGTGGCTTTGAATCCCCCGATA
 ATGGCCTGAAAACATATATGCGTTCTACTGTCATCATTAGCGACATATTGT
 TTTACTTTTCTGCAGTAATATACTTTACTAAGTGGCTTGGTAGATATCGAA
 ACCAGTCGCCCATAGGACAATCTATTGCGGCATCAGCGATTTTGTTC AAC
 CTTTCAATTAATGCTCATTGACCATGGGCCTTTCAATATAATTCAGTCATGC
 TTGGCCTTACTGCTTATGCCATAAATACTTATTAGATGAGTATTATGCTA
 TGGCGGCCGTTTGTGTTTGTCTATCCATTTGTTTTAAACAAATGGCATTGTA
 TTATGCACCGATTTTTTTTTGCTTATCTATTAAGTCGATCATTGCTGTTCCCC
 AAATTTAACATAGCTAGATTGACGGTTATTGCGTTTGCAACACTCGCAACT
 TTTGCTATAATATTTGCGCCATTATATTTCTTGGGAGGAGGATTAAAGAAT
 ATTCACCAATGTATTCACAGGATATTCCTTTTGCCAGGGGCATCTTCGAA
 GACAAGGTTGCTAACTTCTGGTGCGTTACGAACGTGTTTGTAAAATACAA
 GGAAAGATTCACTATACAACAACTCCAGCTATATTCATTGATTGCCACCGT
 GATTGGTTTCTTACCAGCCATGATAATGACATTACTTCATCCCAAAAAGCA
 TCTTCTCCCATACGTGTTAATCGCATGTTTCGATGTCCTTTTTTCTTTTAGC
 TTTCAAGTACATGAGAAAACATCCTCATCCCCTTTTGCCTATTACACTA
 CTCTACTCCTCTACTGATTGGAATGTTCTATCTCTTGTAAGTTGGATAAAC
 AATGTGGCTTTGTTTACGCTATGGCCTTTGTTGAAAAAGGACGGTCTTCAT
 TTACAGTATGCCGTATCTTTCTTACTAAGCAATTGGCTGATTGGAAATTC
 AGTTTTATTACACCAAGGTTCTTGCCAAAATCTTTAACTCCTGGCCCTTCT
 ATCAGCAGCATCAATAGCGACTATAGAAGAAGAAGCTTACTGCCATATAA
 TGTGGTTTGGAAAAGTTTTATCATAGGAACGTATATTGCTATGGGCTTTTA
 TCATTTCTTAGATCAATTTGTAGCACCTCCATCGAAATATCCAGACTTGTG
 GGTGTTGTTGAACTGTGCTGTTGGGTTCAATTGCTTTAGCATATTTTGGCTA
 TGGTCTTATTACAAGATATTCATTCCGGTAGCAAATCCATGAAGGACTTG
 TAG

S. cerevisiae ALG6p

MAIGKRLLVNKPAEESFYASPMYDFLYPFRPVGNQWLPEYIIFVCAVILRCTIG
 LGPYSGKGSPLYGDFAQRHWMEITQHLPLSKWYWYDLQYWGLDYPLTA
 FHSYLLGLIGSFFNPSWFALEKSRGFESPDNGLKTYMRSTVIISDILFYFPAVIY
 FTKWLG RYRNQSPIGQSI AASAILFQPSLMLIDHGHFQYNSV MLGLTAYAINN
 LLDEYYAMA A VCFVLSICFKQMALYYAPIFFAYLLSRSLLPKFN IARLTVI AF
 ATLATFAIIFAPLYFLGGGLKNIHQCIHRIFFARGIFEDK VANFWCVTNV FVK
 YKERFTIQQLQLYSLIATVIGFLPAMIMTLLHPKKHLLPYVLIACSMSFFLFSFQ
 VHEKTILP LLPITLLYSSTDWNVLSLVSWINNVALFTLWPLLK KDGLHLQYA
 VSFLLSNWLIGNFSFITPRFLPKSLTPGPSISSINS DYRRSLLPYNV VWKSFIIGT
 YIAMGFYHFLDQFVAPPSKY PDLWVLLNCAVGFICFSIFWLWSYYKIFTSGSK
 SMKDL

FIGURE 26

P. pastoris ALG6

ATGCCACATAAAAGAACGCCCTCTAGCAGTCTGCTGTATGCAAGAATTCC
 AGGGATCTCTTTTGAAAACCTCTCCGGTGTGGATTGTTTGTCTCCTTTTGA
 CCCGCTCCTAATCAATGGGTAGCACGATACATCATCATCTTTGCAATT
 CTCATCAGATTGGCAGTTGGGCTGGGCTCCTATTCCGGCTTCAACACCCCT
 CCAATGTATGGGGATTTTGAAGCTCAGAGGCATTGGATGGAAATTACTCA
 GCATTTATCCATAGAAAAATGGTACTTCTACGACTTGCAATATTGGGGGCT
 TGACTATCCTCCCTTGACAGCCTTTCATTCATACTTCTTTGGCAAATTAGGC
 AGCTTCATCAATCCAGCATGGTTTGTCTTAGACGTCTCCAGAGGGTTTGAA
 TCAGTGGATCTAAAATCGTACATGAGGGCGACCGCAATTCTCAGTGAGCT
 GTTATGTTTTATTCCAGCTGTCATTTGGTATTGTCGTTGGATGGGACTTAAC
 TACTTCAATCAAAACGCCATTGAGCAAACATAATAGCGTCTGCTATTCTT
 TTCAATCCATCTTTAATTATCATAGATCATGGCCACTTCCAGTACAACCTCA
 GTTATGCTAGGTTTTGCTTTATTATCCATATTAAATCTGTTGTACGATAATT
 TTGCATTAGCGGCTATTTTTTTCGTTCTTTCAATAAGCTTTAAGCAAATGGC
 TCTCTATTATAGCCCCATCATGTTTTTTTACATGCTGAGTGTGAGTTGTTGG
 CCTTTGAAAAACTTCAACTTGTTGAGATTGGCTACTATCAGTATTGCAGTA
 CTCTTGACTTTTGCAACTCTATTACTGCCTTTTGTATTAGTAGATGGGATGT
 CACAAATTGGCCAAATATTATTCAGAGTTTTCCCGTTTTCAAGAGGCTTGT
 TTGAGGATAAGGTGGCCAACTTTTGGTGTACAACGAATATACTGGTAAAG
 TACAAACAGTTATTCAGTACAAAACCCCTTACTAGGATATCGCTAGTAGC
 AACTTTGATTGCAATTAGTCCGTCTTGCTTCATCATTTTTTACTCACCCAAAG
 AAGGTTTTACTACCGTGGGCTTTTGCTGCTTGCTCTTGGGCGTTCTATCTTT
 TCTCTTTCCAAGTCCACGAGAAATCAGTTTTAGTTCCATTGATGCCTACCA
 CTCTATTACTGGTAGAAAAAGACTTGGACATCATCTCAATGGTCTGCTGGA
 TTTCTAATATTGCCTTCTTCAGCATGTGGCCTCTATTAAAAAGAGACGGGC
 TGGCTTTGGAATATTTTGTCTTGGAATATTGAGTAATTGGCTGATTGGAA
 ACCTCAATTGGATTAGTAAATGGCTTGTCCTCCAGTTTCTGATTCCAGGGC
 CTACTCTCTCCAAAAAAGTTCCTAAAAGAGATACTAAAACAGTTGTTTCAT
 ACTCACTGGTTTTGGGGGTCAGTAACATTCGTTTCATACCTCGGAGCTACA
 GTTATCCAGTTCGTAGATTGGCTGTACCTTCCACCTGCCAAGTATCCAGAT
 TTGTGGGTATTTTGAACACTACATTGTCGTTTGCTTGTTTCGGGTTGTTTT
 GGCTATGGATTAACATACTGTACATTTTGCGTGATTTTAAGCTTAAAG
 ATGCTTAG

P. pastoris Alg6

MPHKRTPSSLLYARIPGISFENSPVDFLSPFGPAPNQWVARYIIIFAILRLAV
 GLGSYSGFNTPPMYGDFEAQRHWMEITQHLSIEKWYFYDLQYWGLDYPPLT
 AFHSYFFGKLGSFINPAWFALDVSRGFESVDLKSVMRATAILSELLCFIPAVIW
 YCRWMGLNYFNQNAIEQTHIASAILFNPSLIIDHGHFQYNSVMLGFAALLSILNL
 LYDNFALAAIFFVLSISFKQMALYYSPIMFFYMLSVSCWPLKNFNLLRLATISI
 AVLLTFATLLLPFVLVDGMSQIGQILFRVFPFSRGLFEDKVANFWCTTNILVK
 YKQLFTDKTLTRISLVATLIAISPSCFIIFTHPKKVLLPWAFACSWAFYLSFQ
 VHEKSVLVPLMPTTLLLVEKDLDIISMVCWISNIAFFSMWPLLKRDGLALEYF
 VLGILSNWLIGNLNWISKWLVPFLIPGPTLSKKVPRDKTKTVVHWHFWGS
 VTFVSYLGATVIQFVDWLYLPPAKYPDLWVILNTTLSFACFGLFWLWYNL
 YILRDFKLKDA

FIGURE 27 (sheet 1)

P. pastoris ALG6 BLAST

Score	E	Sequences producing significant alignments:	(bits)	Value
<u>gi 1420090 emb CAA99190.1 </u>		ORF YOR002w [Saccharomyces cerev...	489	e-137
<u>gi 7490584 pir T40396</u>		glucosyltransferase - fission yeast ...	369	e-101
<u>gi 19921070 ref NP_609393.1 </u>		CG5091-PA [Drosophila melanoga...	47	4e-64
<u>gi 15240920 ref NP_198662.1 </u>		glucosyltransferase-like prote...	244	3e-63
<u>gi 7019325 ref NP_037471.1 </u>		dolichyl-P-Glc:Man9GlcNAc2-PP-d...	238	2e-61
<u>gi 12002040 gb AAG43163.1 </u>		AF063604 1 brain my046 protein [H...	236	7e-61
<u>gi 1176671 sp Q09226 ALG6 CAEEL</u>		Probable dolichyl pyrophosph...	222	9e-57
<u>gi 21302638 gb EAA14783.1 </u>		agCP4617 [Anopheles gambiae str....	219	8e-56
<u>gi 5441788 emb CAB46771.1 </u>		probable glucosyltransferase [Sc...	192	1e-47
<u>gi 13129070 ref NP_076984.1 </u>		hypothetical protein MGC2840 s...	112	1e-23
<u>gi 2996578 emb CAA12176.1 </u>		glucosyltransferase [Homo sapiens]	112	1e-23
<u>gi 20835439 ref XP_131506.1 </u>		similar to Dolichyl pyrophosph...	104	3e-21

Alignments

S. cerevisiae

Score = 489 bits (1259), Expect = e-137

Identities = 274/530 (51%), Positives = 358/530 (67%), Gaps = 5/530 (0%)

Query: 20 SFENSPVDFLSPFGPAPNQWVXXXXXXXXXXXXXXXXXVGLGSYSGFNTPPMYGDFEAQRH 79
 SF SP++DFL PF P NQW+ +GLG YSG +PP+YGDFFEAQRH
 Sbjct: 16 SFYASPMYDFLYPFRPVGNQWLPEYIIIFVCAVILRCTIGLGPYSGKGSPLYGDFFEAQRH 75

Query: 80 WMEITQHLSEIKWYFYDLQYWGLDYPPLTAFHSYFFGKLGSFINPAWFALDVSRGFESVD 139
 WMEITQHL + KKY+YDLQYWGLDYPPLTAFHSY G +GSF NP+WFAL+ SRGFES D
 Sbjct: 76 WMEITQHLPLSKWYWDYDLQYWGLDYPPLTAFHSYLLGLIGSFFNPSWFALEKSRGFESPD 135

Query: 140 --LKS YMRATAILSELLCFIPAVIWCYRWMGLNMFNQNAIEQTIIASAILFNPSLIIDH 197
 LK+YMR+T I+S++L + PAVI++ +W+G Y NQ+ I Q+I ASAILF PSL++IDH
 Sbjct: 136 NGLKTYMRSTVLIISDILFYFPAVIYFTKWLG-RYRNQSPIGQSIASAILFQPSLMLIDH 194

Query: 198 GHFQYNSVMLGFALLSILNLLYDNFALAAIFFVLSISFKQMALYYSPIMFFYMLSVSCWP 257
 GHFQYNSVMLG +I NLL + +A+AA+ FVLSI FKQMALYY+PI F Y+LS S
 Sbjct: 195 GHFQYNSVMLGLTAYAINNLLDEYYAMAACVFLSICFKQMALYYAPIFFAYLLSRSL- 253

Query: 258 LKNFNLLRLATISIAVLLTFATLLLP-FVLVDGMSQIGQILFRVFPFSRGLFEDKVANFW 316
 FN+ RL I+ A L TFA + P + L G+ I Q + R+FPF+RG+FEDKVANFW
 Sbjct: 254 FPKFNIA RLTVIAFATLATFAIIIFAPLYFLGGGLKNIHQCIHRIFPFARGIFEDKVANFW 313

Query: 317 CTNINLVKYKQLFTDKTLTRISLVATLIAISPSCFIIFTHPKKVLLPWAFACSWAFYLF 376
 C TN+ VKYK+ FT + L SL+AT+I P+ + HPKK LLP+ ACS +F+LF
 Sbjct: 314 CVTNVVFVKYKERFTIQQLQLYSLIATVIGFLPAMIMTLLHPKKHLLPYVLIACSMSFFLF 373

Query: 377 SFQVHEKSXXXXXXXXXXXXXKDLDIISMVCWISNIAFFSMWPLLKRDGLALEYFVLGI 436
 SFQVHEK+ D +++S+V WI+N+A F++WPLLK+DGL L+Y V +
 Sbjct: 374 SFQVHEKTILIPLLPITLLYSSTDWNVLSLVSWINNVALFTLWPLLKKDGLHLQYAVSFL 433

Query: 437 LSNWLIGNLNWISKWLVPSFLIPGPTLSKKVKPRDTKTVVHTHWFGSVTFVSYLGATVI 496
 LSNWLIGN ++I+ +P L PGP++S +++++ + W S +Y+
 Sbjct: 434 LSNWLIGNFSFITPRFLPKSLTPGPSISSINSIDYRRRSLLPYNVVWKSFIIGTYIAMGFY 493

FIGURE 27 (sheet 2)

Query: 497 QFVDWLYLPPAKYPDLWVILNTTSLFACGLFWLWINYNLYILRDFKLKD 546
 F+D PP+KYPDLWV+LN + F CF +FWLW Y ++ +KD
 Sbjct: 494 HFLDQFVAPPSKYPDWVLLNCAVGFICFSIFWLWSYKIFTSGSKSMKD 543

S. pombe

Score = 369 bits (946), Expect = e-101
 Identities = 228/513 (44%), Positives = 315/513 (61%), Gaps = 35/513 (6%)

Query: 21 FEN-SPVDFLSPFGPAPNQVWXXXXXXXXXXXXXXXXXVGLGSYSGFNTPPMYGDFEAQRH 79
 FEN +PV F+S F +++++ + +G YSG+NTPPMYGDFEAQRH
 Sbjct: 5 FENGAPVQQFVSRFRSYSSKFLFFPCLIMSLVFMQWLISIGPYSGYNTPPMYGDFEAQRH 64

Query: 80 WMEITQHLSIEKWYFYDLQYWGLDYPLTAFHSYFFGKLGS-FINPAWFALDVSRGFESV 138
 WME+T H + +WYF DLQ+WGLDYPLTA+ S+FFG +G F NP WFA SRGFES+
 Sbjct: 65 WMELTLHTPVSQWYFRDLQWGLDYPLTAYVSWFFGIIGHYFFNPEWFADVTSRGFESL 124

Query: 139 DLKSYMRTAILSELLCFIPAVIWCYCRMGLNYFNQNAIEQTIIASAILFNPSLIIDHG 198
 +LK +MR+T I S LL +P +++Y +W N +++ +LF P+L++IDHG
 Sbjct: 125 ELKLFMRSTVIASHLLILVPPLMFYSKWSRRI--PNFVDRNASLIMVLFQPALLLIDHG 182

Query: 199 HFQYNSVMLGFALLSILNLLYDNFALAAIFEVLSISFKQMALYYSPIMFFYMLSVCWPL 258
 HFQYN VMLG + +I NLL + + A FF L+++FKQMALY++P +FFY+L P
 Sbjct: 183 HFQYNCVMLGLVMYAIANLLKNQYVAATFFFCALTFKQMALYFAPPIFFYLLGTCVKPK 242

Query: 259 KNFNLLRLATISIAVLLTFATLLPFVLVDGMSQIGQILFRVFPFSRGLFEDKVANFWCT 318
 F+ R +S+ V+ TF+ +L P++ +D + + QIL RVFPF+RGL+EDKVANFWCT
 Sbjct: 243 IRFS--RFILLSVTVVFTFSLILFPWIYMDYKTLLPQILHRVFPFARGLWEDKVANFWCT 300

Query: 319 TNILVKYQLFDTKTLTRISLVATLIAISPCSFIIIFTHPKKVLLPWAFACSWAFYLF 378
 N + K +++FT L ISL+ TLI+I PSC I+P +P+K LL FA+ SW F+LFSF
 Sbjct: 301 LNTVFKIREVFTLHQLQVISLIFTLISILPSCVILFLYPRKRLALGFASASWGFFLF 360

Query: 379 QVHEKSXXXXXXXXXXXXXKDLDIISMVCWISNIAFFSMWPLLKRDGLALEYFVLGILS 438
 QVHEKS ++ + +N+A FS+WPLLK+DGL L+YF L ++
 Sbjct: 361 QVHEKSVLLPLLPTSILLCHGNITTKPWIALANNLAVFSLWPLLKDKDGLGLQYFTLVLMW 420

Query: 439 NWLIGNLNWISKWLVPFLIPGPTLSKKVPKRDTKTVVHTHWFGSVTFVSYLGATVIQF 498
 NW IG++ SK ++ F + Y+G VI
 Sbjct: 421 NW-IGDMVVFSKNVLF-----IQLSFYVGMIVILG 451

Query: 499 VDWLYLPPAKYPDLWVILNTTSLFACGLFWLW 531
 +D PP++YPDLWVILN TLSFA F +LW
 Sbjct: 452 IDLFIPPPSRYPDLWVILNVTLSFAGFFTIYLW 484

D. melanogaster

Score = 247 bits (630), Expect = 4e-64
 Identities = 175/490 (35%), Positives = 267/490 (54%), Gaps = 55/490 (11%)

Query: 57 VGLGSYSGFNTPPMYGDFEAQRHWMEITQHLSIEKWYF---YDLQYWGLDYPLTAFHS 112
 + L SYSGF++PPM+GD+EAQRHW EIT +L++ +WY DLQYWGLDYPLTA+HS
 Sbjct: 19 ISLYSYSGFDSPPMHGDYEAQRHWQEITVNLAUGEYTNSSNNDLQYWGLDYPLTAYHS 78

Query: 113 YFFGKLGSFINPAWFALDVSRGFESVDLKSVMRTAILSELLCFIPAVIWCYCRMGLNYF 172
 Y G++G+ I+P + L SRGFES + K +MRAT + +++L ++PA++ + +
 Sbjct: 79 YLVGRIGASIDPRFVELHKS RGFESKEHKRFMRATVVSADVLIYLPAMLLLAYSLDKAFR 138

FIGURE 27 (sheet 3)

Query: 173 NQNAIEQTIIASAILFNPSLIIIDHGHFQYNSVMLGFALLSILNLLYDNFALAAIFFVLS 232
 + + + + +A P +ID+GHFQYN++ LGFA ++I +L F AA FF L+
 Sbjct: 139 SDDKFLFLTLVAAY---PGQTLIDNGHFQYNNISLGFAAVAIAAILRRRFYAAAFFFTLA 195

Query: 233 ISFKQMALYYSPIMFFYMLSVCWPLKNFN--LLRLATISIAVLLTFATLLLPPFVLVDGM 290
 +++KQM LY+S + FF L C K+F + ++ I+ VL TFA L +P+ + +
 Sbjct: 196 LNYKQMELYHS-LPFFAFLLGECVSQKSFASFIAEISRIAADVLTGTFAILWVPW--LGSL 252

Query: 291 SQIGQILFRVFPFSRGLFEDKVANFWCTTNILVKYKQLFTDKTLTRISLVATLIAISPS 350
 + Q+L R+FP +RG+FEDKVAN WC N++ K K+ ++ + + + TLIA P+
 Sbjct: 253 QAVLQVLHRLFPVARGVFEDKVANVCAVNVVWKLKHHISNDQMALVCIACITLIASLPTN 312

Query: 351 FIIFTHPKKVLLPWAFACSWAFYLFQVHEKSXXXXXXXXXXXXXKDLDIISMVCW- 409
 ++F V A S AF+LFSFQVHEK+ + + CW
 Sbjct: 313 VLLFRRRTNVGFLALFNTSLAFFLFSFQVHEKTILLTALPA-----LFLKWCWP 362

Query: 410 -----ISNIAFFSMWPLLKRDLGLALEYFVLGILSNWLIGNLNWISKWLVPFSLIPGPTLS 464
 + FSM PLL RD L + V + + + + SK LS
 Sbjct: 363 DEMILFLEVTVFSMLPLLARDELLVPAVVATVAFHLIFKCFDSKSK-----LS 410

Query: 465 KKVPKRDTKTIVHTHFWGSVTFVSYLGAIVQFVDWLYLP-PAKYPDLWVILNTTSLFA 523
 + P + + + + +S + A+ L +P P KYPDLW ++ + S
 Sbjct: 411 NEYPLKYIANI-----SQILMISVVVAS-----LTVPAPTKYPDWPLIISVTSCG 456

Query: 524 CFGLFWLWIN 533
 F LF+LW N
 Sbjct: 457 HFFLFFLWGN 466

A. thaliana

Score = 244 bits (622), Expect = 3e-63
 Identities = 187/488 (38%), Positives = 248/488 (50%), Gaps = 39/488 (7%)

Query: 62 YSGFNTPPMYGDFEAQRHWMEITQHLSIEKWY---FYDLQYWGLDYPPLTAFHSYFFGK 117
 YSG PP +GDFAQRHWMEIT +L + WY + DL YWGLDYPPLTA+ SY G
 Sbjct: 61 YSGAGIPPKFGDFAQRHWMEITTNLPVIDWYRNGTYNDLTYWGLDYPPLTAYQSYIHGI 120

Query: 118 LGSFINPAWFALDVSRGFESVDLKSVMRATAILSELLCFIPAVIWCYCRWMGLNYFNQNAI 177
 F NP AL SRG ES K MR T + S+ F PA +++ N
 Sbjct: 121 FLRFFNPESVALLSSRGHESYLGLLMRWTVLSSDAFIFFPAALFFVLVYHRNRTRGGKS 180

Query: 178 EQTIIASAILFNPSLIIIDHGHFQYNSVMLGFALLSILNLLYDNFALAAIFFVLSISFKQ 237
 E + IL NP LI+IDHGHFQYN + LG + +I +L ++ L + F L++S KQ
 Sbjct: 181 EVAWHIAMILLNPCLILIDHGHFQYNCISLGLTVGAIAAVLCESEVLTCVLFSLALSHKQ 240

Query: 238 MALYYSPIMFFYMLSVCWPLKNFNLLRLATISIAVLLTFATLLLPPFVLVDGMSQIGQIL 297
 M+ Y++P F ++L C K+ +L + + IAV++TF P+ V + +L
 Sbjct: 241 MSAYFAPAFFSHLLG-KCLRRKS-PILSVIKLGIAVIVTFVIFWWPY--VHSLDDFLMVL 296

Query: 298 FRVFPFSRGLFEDKVANFWCTTNILVKYKQLFTDKTLTRISLVATLIAISPSFCIIFTHP 357
 R+ PF RG++ED VANFWCTT+IL+K+K LFT ++L ISL AT++A PS P
 Sbjct: 297 SRLAPFERGIYEDYVANFWCTTSILIKWKNLFTTQSLKSISLAATILASLPSMVQQILSP 356

Query: 358 KKVLLPWAFACSWAFYLFQVHEKSXXXXXXXXXXXXXKDLDIISMVCWISNIAFFS 417
 + S AFYLFQVHEKS L + ++ A FS
 Sbjct: 357 SNEGFLYGLLNSSMAFYLFQVHEKSILMPFLSATLLA----LKLDPHFHSHLTYYALFS 412

FIGURE 27 (sheet 4)

Query: 418 MWPLLKRDGLALEYFVLGILSNWLI---GNLNWISKWLVPSFL---IPGPTLSKKVPKRD 471
 M+PLL RD L + Y L L + GN + I K V F PG
 Sbjct: 413 MFPLLCRDKLLIPYLTLSFLFTVIYHSPGNHHAIQKTDVSFFSFKNFPGYVF----- 464

Query: 472 TKTVVHTHWFWGSVTFVSYLGATVIQFVDWLYLPPAKYPDLWVILNTTLSFACFGLFWLW 531
 ++ TH+F V V YL PP KYP L+ L L F+ F +F +
 Sbjct: 465 ---LLRTHFFISVVLHVLYLTIK-----PPQKYPFLFEALIMILCFSYFIMFAFY 511

Query: 532 INYNLYIL 539
 NY + L
 Sbjct: 512 TNYTQWTL 519

FIGURE 28

K. lactis ALG6

ATCTCTGTTTCAACAGCTCTTGCATTCAATTGGTTCTTTTCGGTCCAATCTATA
TCTTTGGAGGATACAAGAAGCTTAGTGCAATCAATGCACAGGATTTTTCCAT
TTGCCAGGGGTATCTTTGAAGATAAAGTTGCGAATTTTTGGTGCGTTTCTA
ATATTTTCATCAAATATAGAAATCTATTCCTCAGAAGGATCTTCAATTAT
ACTCATTACTCGCAACAGTTATTGGGCTTTTACCATCATTCAATTATAACAT
TTTTATACCCGAAGAGACATTTACTACCATATGCTTTGGCCGCATGTTTCGA
TGTCATTCTTCTTATTTCAGCTTCCAGGTTTCATGAAAAGACAATCTTATTAC
CTTTACTTCCTATTACACTCTTGTACACGTCAAGAGATTGGAATGTTCTAT
CATTGGTTTGTGGATTAACAACGTGGCATTGTTTACACTCTGGCCATTAC
TGAAAAAGGACAATCTAGTATTGCAATATGGAGTCATGTTTCATGTTTAGC
AATTGGTTGATCGGTAACCTTCAGTTTCGTCACACCACGCTTCCTCCCAAAA
TTTTTGACACCAGGGCCATCCATCAGTGATATAGATGTTGATTATAGACGG
GCAAGTTTACTACCCAAGAGCCTAATATGGAGATTAATCATTGTTGGCTCA
TATATTGCAATGGGGATTATTCATTTTCTAGACTATTACGTCTCCCCGCCA
TCAAAATACCCTGATTTATGGGTGCTTGCCAATTGTTCTTGGGCTTCTCA
TGTTTTGTGACATTTTGGATATGGAACAATTATAATTATTCGAAATGAGAA
ACAGCACTTTGCAAGATTTA

K. lactis Alg6p

ISVSTALAFIGSFGPIYIFGGYKNLVQSMHRIFPFARGIFEDKVANFWCVSNIFIK
YRNLFTQKDLQLYSLLATVIGLLPSFIITFLYPKRHLLPYALAACSMSSFLLFSFQ
VHEKTILLPLLPITLLYTSRDWNVLSLVCWINNVALFTLWPLLKKDNLVLQYG
VMFMFSNWLIGNFSFVTPRFLPKFLTPGPSISDIDVDYRRASLLPKSLIWRLIIV
GSYIAMGIIHFLDYYVSPPSKYPDLWVLANCSLGFSCFVTFWIWNNYNYSKZE
TALCKI

FIGURE 29 (sheet 1)

K. lactis ALG6 BLAST

Score E
Sequences producing significant alignments: (bits) Value

gi 1420090 emb CAA99190.1	ORF YOR002w [Saccharomyces cerev...	392	e-108
gi 7490584 pir T40396	glucosyltransferase - fission yeast ...	187	2e-46
gi 15240920 ref NP_198662.1	glucosyltransferase-like prote...	117	2e-25
gi 7019325 ref NP_037471.1	dolichyl-P-Glc:Man9GlcNAc2-PP-d...	103	2e-21
gi 12002040 gb AAG43163.1	AF063604.1 brain my046 protein [H...	102	8e-21
gi 19921070 ref NP_609393.1	CG5091-PA [Drosophila melanoga...	101	1e-20

Alignments

S. cerevisiae

Score = 392 bits (1006), Expect = e-108
Identities = 182/280 (65%), Positives = 218/280 (77%), Gaps = 1/280 (0%)
Frame = +1

```

Query: 1   ISVSTALAFIGSFGPIYIFGG-YKNLVQSMHRIFPFARGIFEDKVANFWCVSNIFIKYRN 177
          I+ +T F F P+Y GG KN+ Q +HRIFPFARGIFEDKVANFWCV+N+F+KY+
Sbjct: 265 IAFATLATFAIIFAPLYFLGGGLKNIHQCIHRIFPFARGIFEDKVANFWCVTNVFKYKE 324

Query: 178 LFTQKDLQLYSLLATVIGLLPSFIITFLYPKRHLLPYALACSMSFFLFSFQVHEKXXXX 357
          FT + LQLYSL+ATVIG LP+ I+T L+PK+HLLPY L ACSMSFFLFSFQVHEK
Sbjct: 325 RFTIQQLQLYSLIATVIGFLPAMIMTLLHPKKHLLPYVLIACSMSFFLFSFQVHEKTILI 384

Query: 358 XXXXXXXXXYSRDNVLSLVCWINNVALFTLWPLLKKDNLVLQYGVFMFMSNWLIGNFSF 537
          Y+S DWNVLSLV WINNVALFTLWPLLKKD L LQY V F+ SNWLIGNFSF
Sbjct: 385 PLLPITLLYSSTDWNVLSLVSWINNVALFTLWPLLKKDGLHLQYAVSFLLSNWLIGNFSF 444

Query: 538 VTPRFLPKFLTPGPSISDIDVDYRRASLLPKSLIWRLIIVGSYIAMGIIHFLDYVSPPS 717
          +TPRFLPK LTPGPSIS I+ DYRR SLLP +++W+ I+G+YIAMG HFLD +V+PPS
Sbjct: 445 ITPRFLPKSLTPGPSISSINSYRRSLLPYNVVWKSFIIGTYIAMGFYHFLDQFVAPPS 504

Query: 718 KYPDLWVLANCSLGFSCFVTFWIWNXYLFEMRNSTLQDL 837
          KYPDLWVL NC++GF CF FW+W+ Y +F + +++DL
Sbjct: 505 KYPDLWVLLNCAVGFIKFSIFWLWSYKIFTSGSKSMKDL 544

```

S. pombe

Score = 187 bits (475), Expect = 2e-46
Identities = 106/280 (37%), Positives = 150/280 (53%), Gaps = 1/280 (0%)
Frame = +1

```

Query: 1   ISVSTALAFIGSFGPIYIFGGYKNLV-QSMHRIFPFARGIFEDKVANFWCVSNIFIKYRN 177
          +SV+ F P +I+ YK L+ Q +HR+FPFARG++EDKVANFWC N K R
Sbjct: 251 LSVTVVFTFSLILFP-WIYMDYKTLLPQILHRVFPFARGLWEDKVANFWCTLNTVFKIRE 309

Query: 178 LFTQKDLQLYSLLATVIGLLPSFIITFLYPKRHLLPYALACSMSFFLFSFQVHEKXXXX 357
          +FT LQ+ SL+ T+I +LPS +I FLYP++ LL A+ S FFLFSFQVHEK
Sbjct: 310 VFTLHQLQVISLIFTLISILPSCVILFLYPRKRLLALGFASASWGFFLFSFQVHEKSVLL 369

```

FIGURE 29 (sheet 2)

Query: 358 XXXXXXXXXYSRDWNVLSLVCWINNVALFTLWPLLKKDNLVLQYGVFMFMSNWLNIGNFSF 537
 + + NN+A+F+LWPLLKKD L LQY + + NW
 Sbjct: 370 PLLPTSILLCHGNITTKPWIALANNLAVFSLWPLLKKDGLGLQYFTLVLMWNW----- 422

Query: 538 VTPRFLPKFLTTPGPSISDIDVDYRRASLLPKSLIWRLIIVGSYIAMGIIHFLDYVSPPS 717
 I D+ V K++++R I + Y+ M +I +D ++ PPS
 Sbjct: 423 -----IGDMVV-----FSKNVLFRIQLSFYVGMIVILGIDLFIPPPS 460

Query: 718 KYPDLWVLANCSLGFSCFVTFWIWNNYXLFEMRNSTLQDL 837
 +YPDLWV+ N +L F+ F T ++W L + + DL
 Sbjct: 461 RYPDLWVILNVTLFAGFFTIYLTWLGRLLHISKLSTDL 500

A. thaliana

Score = 117 bits (292), Expect = 2e-25
 Identities = 81/240 (33%), Positives = 120/240 (50%), Gaps = 2/240 (0%)
 Frame = +1

Query: 85 MHRIFPFARGIFEDKVANFWCVSNIFIKYRNLFTQKDLQLYSLLATVIGLLPSFIITFLY 264
 + R+ PF RGI+ED VANFWC ++I IK++NLFT + L+ SL AT++ LPS + L
 Sbjct: 296 LSRLAPFERGIYEDYVANFWCTTSILIKWKNLFTTQSLKSISLAATILASLPSMVQQILS 355

Query: 265 PKRHLLPYALAACSMSSFFLFSFQVHEKXXXXXXXXXXXXXXYSRDWNVLSLVCWINNVALF 444
 P Y L SM+F+LFSFQVHEK + L + ALF
 Sbjct: 356 PSNEGFLYGLLNSSMAFYLFSSFQVHEKSILMPFLSATLLALKLPDHFSLTY--ALF 411

Query: 445 TLWPLLKKDNLVLQYGVFMFMSNWLNIGNFSFVTPRFLPKFLTTPG--PSISDIDVDYRRAS 618
 +++PLL +D L++ Y + SF+ F + +PG +I DV +
 Sbjct: 412 SMFPLLCRDKLLIPYLT-----SFL---FTVIYHSPGNHHAIQKTDVSFFSFK 457

Query: 619 LLPKSLIWRLIIVGSYIAMGIIHFLDYVSPPSKYPDLWVLANCSLGFSCFVTFWIWNNY 798
 P + L+ +I++ ++H L + PP KYP L+ L FS F+ F + NY
 Sbjct: 458 NFPGYVF--LLRTHFFISV-VLHVLYLTIKPPQKYPFLFEALIMILCFSYFIMEFYTN 514

H. sapiens

Score = 103 bits (258), Expect = 2e-21
 Identities = 78/266 (29%), Positives = 123/266 (46%), Gaps = 3/266 (1%)
 Frame = +1

Query: 7 VSTALAFIGSFPGPIYI--FGGYKNLVQSMHRIFPFARGIFEDKVANFWCVSNIFIKYRNL 180
 V A + SF ++ F + +Q + R+FP RG+FEDKVAN WC N+F+K +++
 Sbjct: 232 VKLACIVVASFVLCWLPFFTEREQTLQVLRRLFPVDRGLFEDKVANIWCSENVFLKIKDI 291

Query: 181 FTQKDLQLYSLLATVIGLLPSFIITFLYPKRHLLPYALAACSMSSFFLFSFQVHEKXXXXX 360
 + + S T + LLP+ I L P + L +C++SFFLFSFQVHEK
 Sbjct: 292 LPRHIQLIMSFCFTFLSLLPACIKLILQPSSKGFKFTLVSCALSFFLFSFQVHEKSILLV 351

Query: 361 XXXXXXXXXYSRDWNVLSLVCWINNVALFTLWPLLKKDNLVLQYGVFMF-FSNWLNIGNFSF 537
 + + + W V+ F++ PLL KD L++ V M F + +FS
 Sbjct: 352 SLPVCLVLS---EIPFMSTWFLLVSTFSMLPLLKDELLMPSVVTMAFFIACVTSFSI 407

Query: 538 VTPRFLPKFLTTPGPSISDIDVDYRRASLLPKSLIWRLIIVGSYIAMGIIHFLDYVSPPS 717
 + SIS V S I + + + S I M ++ + + PP
 Sbjct: 408 FEKTSEEELQLKSFSIS---VRKYLPCFTFLSRIIQYLFLISVITMVLTLTMTVTLDP 464

Query: 718 KYPDLWVLANCSLGFSCFVTFWIWNN 795
 K PDL+ + C + F+ F ++ N
 Sbjct: 465 KLPDLFSVLVCFVSCNLNFFLVYFN 490

FIGURE 30

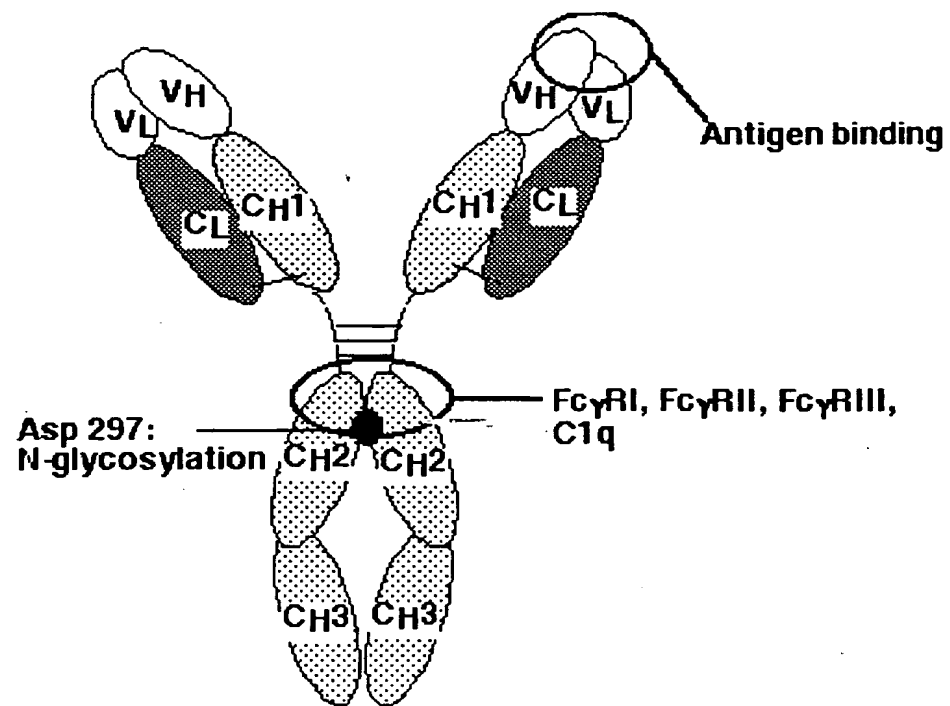


FIGURE 31

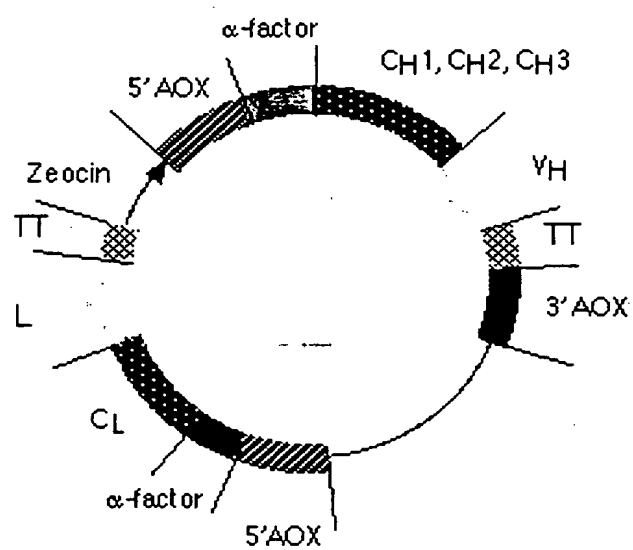


FIGURE 32

>gi|6754685|ref|NM_010795.1| Mus musculus mannoside acetyl
glucosaminyltransferase 3 (Mgat3), mRNA

ATGAAGATGAGACGCTACAAGCTCTTTCTCATGTTCTGTATGGCTGGCCTGTGCCTCATATCCTTCCTGC
ACTTCTTTAAGACCTTATCCTATGTACCTTCCCCGAGAGAACTGGCCTCCCTCAGCCCTAACCTCGTATC
CAGCTTCTTCTGGAACAATGCCCTGTCACTCCCCAGGCCAGTCCGGAGCCGGGTGGCCCCGACCTATTG
CGGACACCCCTCTACTCCCACTCTCCCTGCTCCAGCCACTGTCCCCGAGCAAGGCCACAGAGGAAGTGC
ACCGGGTGGACTTCGTGTTGCCGGAGGACACACGGAGTATTTGTGCGCACCAAGCTGGTGGTGTGTG
CTTCAAACCAAGGTACCAGGATGCTGGAGAAACCTTCGCCAGGGCGGACAGAGGAGAAGCCCCGAAGTGTCT
GAGGGCTCCTCAGCCCCGGGGACCTGCTCGGAGGCCCATGAGGCACGTGTTGAGTACGCGGGAGCGCCTGG
GCAGCCGGGGCACTAGGCGCAAGTGGGTTGAGTGTGTGTGCTGCCAGGCTGGCACGGGGCCAGTTGCGG
GGTGGCCACGGTGGTGCAGTATTCCAACCTGCCACCAAGGAACGCCTGGTACCCAGGGAGGTACCGAGG
CGGGTTATCAACGCCATCAACATCAACCACGAGTTTCGACCTGCTGGATGTGCGCTTCCATGAGCTGGGAG
ATGTTGTGGACGCCTTCGTGGTCTGTGAATCTAATTTACCCGCTACGGGGAGCCTCGGCCGCTCAAGTT
CCGAGAGATGCTGACCAATGGCACCTTCGAGTACATCCGCCACAAGGTGCTCTATGTCTTCCTGGACCAT
TTCCACCTGGTGGCCGTGAGGACGGCTGGATTGCGGATGACTACCTGCGCACCTTCCTCACCCAGGATG
GCGTCTCCCGCCTGCGCAACCTGCGGCCCGATGACGTCTTTATCATCGACGATGCGGACGAGATCCCTGC
GCGTGATGGTGTGCTGTTCTCAAACCTCTACGATGGCTGGACAGAGCCCTTCGCCTTCCACATGCGGAAG
TCCCTGTATGGTTTCTTCTGGAAGCAGCCGGGCACACTGGAGGTGGTGTGAGGCTGCACCATGGACATGC
TGCAGGCCGTGTATGGGCTGGATGGCATCCGCCTGCGCCGCCAGTACTACACCATGCCCAACTTCCG
GCAGTATGAGAACCACCGCCACATCCTAGTGCAGTGGTCTCTCGGCAGCCCCCTGCACTTCGCGGGC
TGGCATTGCTCCTGGTGTCTTACACCCGAGGGCATCTACTTTAAACTCGTGTGAGCCAGAAATGGCGACT
TCCCCCGCTGGGGTGACTATGAGGACAAGAGGGACCTCAATTACATCCGCAGCTTGATCCGCACTGGGGG
ATGGTTTCGACGGAACGCAGCAGGAGTACCCTCCTGCGGACCCAGTGAGCACATGTATGCTCCTAAATAC
CTGCTCAAGAACTATGACCAGTTCCGCTACTTGCTGGAAAATCCCTACCGGGAGCCCAAGAGCACTGTAG
AGGGTGGGCGCCAGAACCAGGGCTCAGATGGAAGGCCATCTGCTGTCAGGGGCAAGTTGGATACAGTGGA
GGGCTAG

>gi|2117717|pir||JC4362 beta-1,4-mannosyl-glycoprotein 4-beta-N-
acetylglucosaminyltransferase (EC 2.4.1.144) III - mouse
MRRYKLFMLFCMAGLCLISFLHFFKTLSTVTFPRELASLSPNLISFFWNNAPVTPQASPEPGDPDLLRT
PLYSHSPLLQPLSPSKATEELHRVDFVLPEDTTEYFVRTKAGGVCFKPGTRMLEKPSGRTEEEKTEVSEG
SSARGPARRPMRHVLSSRERLGSRGTRRKWVECVCLPGWHGPSCGVPTVVQYSNLPKTERLVPREVP
INAININHEFDLLDVRFHGELGDVVDFAFVVCDSNFTAYGEPRLKFRMLTNGTFEYIRHKVLYVFLDHFP
PGGRQDGIADDDYLRFTLTQDGVSRRLRLRPDDVFIIDDADEIPARDGVLFLKLYDGTWTEPF AFHMRKSL
YGF FWKQPGTLEVVS GCTMDMLQAVYGLDGIRLRRRQYYTMPNFRQYENRTGHLVQWSLGSPLH FAGWH
CSWCFTPEGIYFKLVSAQNGDFPRWGDYEDKRD LNYIRSLIRTGGWFDGTQQEYPPADPSEHMYAPKYL
KNYDQFRYLLNPYREPKSTVEGGRQNQGS DGRSSAVRGKLDTAEG

FIGURE 33

>gi|6912501|ref|NM_012214.1| Homo sapiens mannosyl
(alpha-1,3-)-glycoprotein beta-1,4-N-
acetylglucosaminyltransferase, isoenzyme A (MGAT4A), mRNA

GAAATGAACCTCTCTTATTGATTTTTATTGGCCTAGAGCCAGGAGTACTGCATTTCAGTTGACTTTCAGG
GTAAAAAGAAAACAGTCCTGGTTGTTGTCATCATAAACATATGGACCAGTGTGATGGTGAAATGAGATG
AGGCTCCGCAATGGAAGTGTAGCCACTGCTTTAGCATTATCACTTCCTTCCTTACTTTGTCTTGAT
ACTACATGGCAAAATGGGAAAGAAAACTGATTGCTTATCAACGAGAATTCCTTGCTTTGAAAGAACGT
CTTCGAATAGCTGAACACAGAATCTCACAGCGCTCTTCTGAATTAATACGATTGTGCAACAGTTCAAG
CGTGTAGGAGCAGAAACAAATGGAAGTAAGGATGCGTTGAATAAGTTTTTCAGATAATACCCTAAAGCTG
TTAAAGGAGTTAACAAGCAAAAAATCTCTTCAAGTGCCAAAGTATTTATTATCATTTGCCTCATTTATTG
AAAAATGAAGGAAGTCTTCAACCTGCTGTACAGATTGGCAACGGAAGAACAGGAGTTTCAATAGTCATG
GGCATTCCCACAGTGAAGAGAGAAGTTAAATCTTACCTCATAGAACTCTTCATTCCCTTATTGATAAC
CTGTATCCTGAAGAGAAGTTGGACTGTGTTATAGTAGTCTTCATAGGAGAGACAGATATTGATTATGTA
CATGGTGTGTAGCCAACCTGGAGAAAGAATTTCTAAAGAAATCAGTTCTGGCTTGGTGGAAGTCATA
TCACCCCTGAAAGCTATTATCCTGACTTGACAAACCTAAAGGAGACATTTGGAGACTCCAAAGAAAGA
GTAAGATGGAGAACAAAGCAAAACCTAGATTACTGTTTTCTAATGATGTATGCTCAAGAAAAGGGCATA
TATTACATTTCAGCTTGAAGATGATATTATTGTCAAACAAAATTATTTTAATACCATAAAAAATTTTGCA
CTTCAACTTTCTTCTGAGGAATGGATGATTCTAGAGTTTCCAGCTGGGCTTCATTGGTAAAATGTTT
CAAGCGCCGGATCTTACTCTGATTGTAGAATTCATATTTCATGTTTTTACAAGGAGAAACCCATTGATTGG
CTCCTGGACCATATTCTCTGGGTGAAAGTCTGCAACCCTGAAAAAGATGCAAAACATTGTGATAGACAG
AAAGCAAATCTGCGAATTCGCTTCAGACCTTCCCTTTTCCAACATGTTGGTCTGCACTCATCACTATCA
GGAAAAATCCAAAACTCACGGATAAAGATTATATGAAACCATTACTTCTTAAATCCATGTAAACCCA
CCTGCGGAGGTATCTACTTCCTTGAAGGTCTACCAAGGGCATACGCTGGAGAAAACCTTACATGGGAGAG
GATTTCTTCTGGGCTATCACACCGATAGCTGGAGACTACATCTTGTTTAAATTTGATAAACACAGTCAAT
GTAGAAAGTTATTTGTTCCATAGCGGCAACCAAGAACATCCTGGAGATATTCTGCTAAACACAACCTGTG
GAAGTTTTGCCTTTTAAGAGTGAAGGTTTGGAAATAAGCAAAGAAACCAAGACAAACGATTAGAAGAT
GGCTATTTTCAAGATAGGAAATTTGAGAATGGTGTGTCAGAAAGGAATGGTGGATCCCAAGTCTCAATCCC
ATTTTCAGCCTTTTCGACTTTTCAGTTATTTCAGAATTCTGCTGTTTGGGCCATTCTTAATGAGATTTCATATT
AAAAAAGCCACCAACTGATCATCTGAGAAACCAACACATTTTTTCTGTGAATTTGTTAATTAAAGATA
GTTAAGCATGTATCTTTTTTTTATTCTACTTGAACACTACCTCTTGTGAAGTCTACTGTAGATAAGAC
GATTGTCATTTCCACTTGGAAAGTGAATCTCCCATATAAATTGTATTTGTTTGAACATAAGCTGTCCTC
AGATTTTAACCTGACTCAAACATTTTTCAATTATGACAGCCTGTTAATATGACTTGTACTATTTTGTA
TTATACTAATAACATAAGAGTTGTACATATTGTTACATTCTTTAAATTTGAGAAAACTAATGTTACATA
CATTTTATGAAGGGGTACTTTTGAGGTTCACTTATTTTACTATT

>gi|6912502|ref|NP_036346.1| mannosyl (alpha-1,3-)-
glycoprotein beta-1,4-N-acetylglucosaminyltransferase,
isoenzyme A; UDP-N-acetylglucosamine:alpha1,3-d-mannoside
beta1,4-N-acetylglucosaminyltransferase; alpha-1,3-
mannosyl-glycoprotein beta-1,4-N-
acetylglucosaminyltransferase [Homo sapiens]

MRLRNGTVATALAFITSFLTLSWYTTWQNGKEKLIAYQREFLALKERLRIAHRISQ
RSSELNTIVQQFKRVGAETNGSKDALNKFSDNTLKLKELTSKKSQVPSIYYHLPH
LLKNEGSLQPAVQIGNRTGVSIVMGIPTVKREVKSyliETLHSLIDNLYPEEKLD
VIVVFIGETDIDYVHGVVANLEKEFSKEISSGLVEVISPPESYYPDLTNLKETFGDS
KERVVRWRTKQNLDYCFLLMYAQEKGIYYIQLEDDIIVKQNYFNTIKNFALQLSSEEW
MILEFSQLGFIGKMFQAPDLTLIVEFIFMFYKEKPIDWLLDHILWVKVCNPEKDAKH
CDRQKANLRIRFRPSLFQHVGLHSSLSGKIQKLTDKDYMKPLLLKIHVNPPAEVSTS
LKVYQGHTLEKTYMGEDFFWAITPIAGDYILFKFDKPVNVESYLFHSGNQEHDPDIL
LNTTVEVLPFKSEGLEISKETKDKRLEDGYFRIGKFENGVAEGMVDPSLNPI SAFRL
SVIQNSAVWAILNEIHIKKATN

FIGURE 34 (sheet 1)

>gi|18997006|gb|AF474154.1| Mus musculus N-acetylglucosaminyltransferase V (Mgat5) mRNA, complete cds

ATTGCTAGAGAGAGATGGCTTTCTTTTCTCCCTGGAAGTTGTCCTCTCAGAAGCTGG
GCTTTTTCTCTGGTGACTTTCGGCTTCATCTGGGGCATGATGCTTCTGCACTTCACCA
TCCAGCAGCGGACTCAGCCCGAGAGCAGCTCCATGTTACGGGAGCAGATCCTTGACC
TCAGCAAGAGGTACATTAAGGCACTGGCAGAGGAGAACAGGGACGTGGTGGATGGCC
CCTACGCTGGTGTTCATGACAGCCTATGATCTGAAGAAAACGCTCGCCGTCTTGCTGG
ATAACATCCTGTCAGCGCATTGGCAAGCTCGAGTCAAAGGTGGACAATCTGGTCAACG
GCACAGGAGCGAACTCCACCAACTCCACCACGGCTGTCCCCAGCTTGGTGTGCGCTTG
AGAAAATTAATGTGGCAGATATCATTAATGGAGTTCAGGAAAAATGTGTATTGCCTC
CTATGGATGGCTACCCCCACTGCGAGGGGAAAATCAAGTGGATGAAGGACATGTGGC
GCTCGGACCCCTGCTACGCAGACTATGGAGTGGACGGGACCTCCTGCTCCTTTTTTA
TTTACCTCAGTGAGGTTGAAAATTGGTGTCTCGTTTACCTTGGAGAGCAAAAAATC
CCTATGAAGAAGCTGATCATAACTCATTGGCGGAAATCCGTACGGATTTTAACATTTC
TCTACGGCATGATGAAGAAGCACGAGGAGTTCCGTTGGATGAGGCTTCGGATCCGGC
GAATGGCTGACGCGTGGATCCAAGCTATCAAGTCTCTGGCGGAGAAACAAAACCTTG
AGAAGAGGAAACGGAAGAAAATCCTTGTTACCTGGGGCTCCTGACCAAGGAATCGG
GCTTCAAGATTGCGGAGACAGCATTTCAGCGGTGGCCCTCTGGGTGAACTCGTTCAGT
GGAGTGACTTAATCACATCTCTGTACCTGCTGGGCCATGACATCCGGATCTCGGCCT
CACTGGCTGAGCTCAAGGAGATAATGAAGAAGGTTGTTGGAAACCGGTCTGGCTGTC
CAACTGTAGGAGACAGAATCGTTGAGCTGATTTATATCGATATTGTGGGACTTGCTC
AATTTAAGAAAACACTAGGGCCATCCTGGGTTTATTACCAGTGCATGCTCCGGGTGC
TAGACTCCTTTGGAACAGAACCTGAGTTCAATCATGCGAGCTATGCCAGTCAAAAG
GCCACAAGACCCCTGGGGAAAGTGAATCTGAACCCGCAGCAGTTTTACACCATGT
TCCCTCATACCCAGACAACAGCTTTCTGGGCTTCGTGGTGGAGCAGCACCTGAACT
CCAGCGACATTACCCACATCAACGAGATCAAAAGGCAGAACCCAGTCCCTTGTGTATG
GCAAAGTGGATAGTTTCTGGAAGAATAAGAAAATCTACCTGGATATCATTCACACGT
ACATGGAAGTGCACGCCACTGTTTATGGCTCCAGTACCAAGAACATTCCCAGTTACG
TGAAAACCATGGCATTCTCAGTGGACGTGACCTGCAGTTTCTTCTCCGGGAAACCA
AGCTGTTCTGTTGGGCTCGGATTCCCTTATGAAGGCCAGCTCCCTTGGAGGCCATCG
CGAATGGATGTGCTTCTCTGAACCCCAAGTTCAACCCTCCCAAAGCAGCAAAAACA
CAGACTTCTTCATTGGCAAGCCAACACTGAGAGAGCTGACATCCCAGCATCCTTACG
CAGAAGTCTTCATCGGCCGGCCACACGTCTGGACTGTGGATCTCAATAACCGAGAGG
AAGTAGAAGATGCAGTAAAAGCCATCTTAAACCAGAAGATTGAGCCGTATATGCCAT
ATGAGTTCACATGTGAAGGCATGCTGCAGAGAATCAACGCTTTTATTGAAAAACAGG
ACTTCTGCCATGGCCAAGTGATGTGGCCGCCCCCTCAGCGCCCTGCAGGTTAAGCTGG
CTGAGCCAGGGCAGTCTTGCAAACAGGTGTGCCAGGAGAGCCAGTCTATCTGCGAGC
CATCCTTCTTTCAACACCTCAACAAGGAAAAGGACCTGCTGAAGTATAAGGTGACCT
GCCAAAGCTCAGAACTGTACAAGGACATCCTGGTGCCCTCCTTCTACCCCAAGAGCA
AGCACTGTGTGTTCCAAGGGGACCTCCTGCTCTTCAGTTGTGCCGGAGCCCATCCCA
CACACCAGCGGATCTGCCCCCTGCCGGGACTTCATCAAGGGCCAAGTGGCCCTCTGCA
AAGACTGCCTATAGCATCGCTGCCCTGAATTAACCTCAGACGGGAAAGACGTGGCTCC
ACTGGGCAGGGCCAAGGGGCACAAAGACATTCAGGGACTCTGACCAGAGCCTGAGAT
CTTTGGTCCAGGGCTTGAGTTTAGTACCGCTCCAGCCACAGCCAGTGCATCCCAGTT
TACACCAAAACCACAAGGGAACAGGTTAGAACAGGAACCTGGGTCTCCTCAGTGTA
AGGAATGTCCTCTCTGTCTGGGAGATCGAGCGACTGTAGGGAAAGGATCCAGGCAGT
TGCTCCCGGGAATTTTTTTTTTTTTTTTTTTTAAAGAAGGGATAAAAGTCCCGAGAC

TCATTCAAACCTGAAAACAAAACAGGAAGAGGGAATTGAGCCAATTGGGAAGGACTTT
GGGGCCGATCCTAAACCAATTAATTTATTTATTTGGGAGGATGGGGGCGGGCTCGGG
AGGGAGGAGAGGGGTTGAACAGTTTCCTTTTGTTCCTCACTGTTAATTCGCCCACCT
TCGGGCCCTTCTTGTTCCTGCAGCGCCAAGCAGGGTGCAGAGGGGCTGTGGCTTGCTT
GAGGGGCCACTGTGGGGCTTCACTCCTGGTCACAGGTGGCAGCAGAGAAAAGAGATG
TCTATAAGCAGGGGGATGTAGCTCAGTTTGTAGAATGCTTGCATAGCATAAATGAAG
TCCTGGGTTCCTATCCCCAGCACCATATAAATGCAGGTAAGAAACAGAGTCAGGAGGA
CCAAGCATTCTCCTTGGCTACATAACAAAAGCAAGGCCTTTGTCCCCATGTCTTGGC
TACAAGAGACCCTATCTCAGAAAATTGTGGGGGGGAGGGGGGGGGAAATGGCCTTGA
AAACACAGCCAGTCACTGTCACTGCATTGCCAGAAGTGGTGGATCCCAGGTGTGCTT
GGCAGATAACAGCTAAAAGGCACATAACCTTGGTGGGGAAATAAATGCCTGTGGTGT
CCTGAGGGCCCCACCAAGTTCCAAAAAAAAAAAAA

>gi|18997007|gb|AAL83249.1|AF474154_1 N-
acetylglucosaminyltransferase V [Mus musculus]

MAFFSPWKLSSQKLGFVLVTFGFIWGMMLLHFTIQQRTQPESSSMLREQILDLSKRY
IKALAEENRDVVDGPYAGVMTAYDLKKTALVLLDNILQIRIGKLESKVDNLVNGTGAN
STNSTTAVPSLVLEKINVADIINGVQEKCVLPMDGYPHCEGKIKWMKDMWRSDPC
YADYGVDGTSCSFFIYLSEVENWCPRLPWRAKNPYEEADHNSLAEIRTDNFNILYGM
KKHEEFRWMRLRIRRMADAWIQAIKSLAEKQNLKRRKKILVHLGLLTKEGFKIA
ETAFSGGPLGELVQWSDLITSLYLLGHDIRISASLAELEIMKKVVGNRSGCPTVGD
RIVELIYIDIVGLAQFKKTLGPSWVHYQCMLRVLDSEFGTEPEFNHASAQAQSKGHKTP
WGKWNLNPPQQFYTMFPHTPDNSFLGFVVEQHLNSSDIHHINEIKRQNSLVYGVKVD
FWKNKKIYLDIIHTYMEVHATVYGSSTKNIPSYVKNHGILSGRDLQFLRETKLFVG
LGFPYEGPAPLEAIIANGCAFLNPKFNPPKSSKNTDFFIGKPTLRELTSQHPYAEVFI
GRPHVWTVDLNNREEVEDAVKAILNQKIEPYMPYEFTCEGMLQRINAFIEKQDFCHG
QVMWPPLSALQVKLAEPGQSQCKQVCQESQLICEPSFFQHLNKEKDLLKYKVTQSS
LYKDILVPSFYPKSKHCVFQGDLLLFSCAGAHPTHQRICPCRDFIKGQVALCKDCL

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